Seguence 1

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DD166084 Treatment
M10065 Human apoli
AF261280 Pan trogl
AC146473 Hylobates
AC145523 Papio ham
AC151887 Saimiri b
                                                                                                                                                                                                              AX33278 Sequence
AX409597 Sequence
M12529 Human apol1
BD064748 Method fo
BD004279 Apo E hum
CQ719877 Sequence
BD084811 Diagnosis
AF261279 Homo sapi
AK285122 Sequence
AR262197 Sequence
AR262197 Methods a
AR262772 Sequence
BD004278 Apo E hum
CQ785970 Sequence
CQ87526 Sequence
CQ86276 Sequence
CQ96136 Sequence
CQ9137 Sequence
DD166083 Treatment
AR380462 Sequence
AX81158 Sequence
K00396 Homo sapien
BC003557 Homo sapien
BC003557 Homo sapien
BC003557 Homo sapien
BC003557 Homo sapien
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AF200502 Gorilla g
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BD004277 Apo E hum
DD166085 Treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 1110)

Teranishi,Y., Takamatsu,N., Matsui,Y., Kimura,M. and Ikeda,Y.
DNA FRAGMENT
PATEMI: JP 1985118189-A 1 25-JUN-1985;
MITSUBISHI CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
JP 1981118189-A/1
25-JUN-1985
29-NOV-1983 JP 1983224980
TERANISHI YUTAKA, TAKAMATSU NOBUHIKO, MATSUI YASUSHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            בטטשב 1110 bp RP
CDNA coding human apolipoprotein E3.
החמזרים
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12N15/00, C07H21/04//C12P21/00;
strandedness: Double;
topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                                               AC146473
AC145523
AC151887
BABAPOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC021988
AF303830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF200497S3
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AR282772
MFAPOE
                                                                                       AR380462
AX821568
HUMAPOE3
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AX409597
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BD004279
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AX358722
AF050154
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HUMAPOE4
AF261280
                                                                                                                             BC003557
AR531680
                                                                                                                                                                  E08423
BD004277
                                                                CQ981476
DD166083
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                                                                                                                                                                                                                                                                                              BD084811
                                                                                                                                                                                                                                           HUMAPOE
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JP 1985118189-A/1.
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Homo sapiens
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PN JP 1985118189-.
PD 25-JUN-1985
PF 29-NOV-1983 JP
PI TERANISHI YUTA,
KIMURA MASAKO,
PI IKEDA YASUKO
PC CI2NIS/00,CO7H;
CC strandedness: I
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91.7 5491
91.7 41907
91.7 107567
91.3 3805
91.0 1178
90.5 5515
88.6 5415
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85.1 183798
84.0 191327
83.1 4762
83.0 208239
80.7 1138
77.1 718
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E00359
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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      Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=Abss/ABSWEBs spool/10509827854/runat 14062006 081825_26727/app_query.fasta_1
-Q=Abss/ABSWEBs spool/10509827854/runat 14062006 081825_26727/app_query.fasta_1
-DB=GenEmbl -OFMT=fastap -SUFFIX=p3n.rge -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -ENN=-1 -MATRIX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -ONORM=Ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=22000000000 -HOST=abss02h
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-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=0 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPEXT=7
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E00823 DNA sequenc
AX302545 Sequence
                                                                                     June 14, 2006, 19:02:13; Search time 9258.62 Seconds (without alignments) 3097.698 Million cell.updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                1 KVEQAVETEPEPELRQQTEW......VEKVQAAVGTSAAPVPSDNH 299
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                                                                                                                                                                                                                                                                                              12732272
               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                              - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                     6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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E00823
AX302545
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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gb_ph:,
gb_ph:,
gb_pr:,
gb_rc:,
gb_yr:,
gb_uv:,
gb_uv:,
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Database :

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Minimum DB e Maximum DB e

Perfect score:

Sequence:

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Scoring table:

PAT 29-SEP-1997

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1493 1493 1493

Score

Result No.

AC021988 Homo sapi AF303830 Tupaia gl

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E00823.1 GI:2169084
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S DPPLIGE.
S DPPLIGE.
S DP 198006997-A/1.
unidentified
unidentified
unidentified
unidentified
unclassified sequences.
Teranishi,Y., Matsui,Y., Ikeda,Y. and Kimura,M.
TEACHISHI,Y., Matsui,Y., Ikeda,Y.
TEACHISHI,Y., Matsui,Y. and Kimura,M.
TEACHISHI,Y., Matsui,Y. and Kimura,M.
TEACHISHI,Y., Matsui,Y. and Kimura,M.
TEACHISHI,Y. and Kimura,M.
TEACHISHI,Y.
TEACHI
                                                                                                                                                                                                                                                                                                                   E00823 1110 bp DNA linear PAT 29-SEP-1997 DNA sequence coding for human apolipoprotein E and its signal peptide.
                                                                849 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCCAGTGGCCGGGCTGGTG 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
1. .1110
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DB:
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                                                                                                                                           261
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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                                                                                                           15. .968
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/product='apolipoprotein B3'
Location/Qualifiers
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299
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69. .965
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
hypothetical: No;
anti-sense: No;
*source: tissue_type=liver;
Location/Qualifiers
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Best Local Similarity:
Query Match:
DB:
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us-09-827-854a-2.p2n.rge

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CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCCAGCTCCCAGGTCACCCCAGGAACTG
                                                                                                                                                                                                                   ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
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Hominidae, Homo.
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Tumor markers in ovarian cancer
Patent: WO 0175177-A 63 11-OCT-2001;
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Sequence 63 from Patent W00175177.
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CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC 474
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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4-Oxo-quinazolines as LXR nuclear receptor binding compounds Patent: EP 1398032-A 11 17-MAR-2004;
PheneX Pharmaceuticals AG (DE)
Location/Qualifiers
1. 1156
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2 bujita, S., Hamanaka, H., Fukui, Y. and Yokoyama, M.

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B Atenti JP 2010177028-A 2 23-JAN-2001;

P A 23-JAN-2001

P P 23-JAN-2001

P P 23-JAN-2001

P P 23-JAN-2001

P P 24-APR-2000 JP 2000128919

P R SHINOBU FULITA, HIROKI HAMANAKA, YUKO FUKUI, MINESUKE YOKOYAMA PC
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Herr, A., Hinzmann, B., Dahl, E., Staub, E., Pilarsky, C. and Specht, T. Human nucleic acid sequences from carcinomas of the bladder Patent: WO 2004076613-A 12 10-58P-2004;
Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE); Staub, Eike (DE); Pilarsky, Christian (DE); Specht, Thomas (DE)
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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Hominidae; Homo.
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                                                                                   GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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                                     GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAppTyrLeuArgTrpVal
                                                                        GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
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261 LeuLysserTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280	Qy         141 LeuargLysLeuargLysArgLeuLeuargAspAspLeuGlnLysArgLeuAla 160           Db         535 CTGGGAAGCTGCGTAAGCGCTCCGGCGATGACCTGCGAGAGACCTGCAGAGACCTGCAGAGACCTGCAGAGACTGCTGCAGAGACTGCTAGAGACTGCTGATGACTGAGAGAGA
GAGAAGGTGCATGCGTGGGCACCAGCGCCCCTGTGCCCAGCGACAATCAC 1011	Db 595 GTGTACAGGCCGGGGCCCGGGGCCCGAGCGCCCTCAGCGCCATCCGCGAGCGC 654  Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
CQ896276 1156 bp DNA linear PAT 05-NOV-2004 Sequence 100 from Patent WO2004076614.	655 CTGGGGCCCCTGGTGGAACAGGCCGCGTGTGTGTTGTGGGTTCCCTTGGCCGGC
2896276 2896276.1 GI:55468125	Oy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Homo sapiens Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,	Oy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValArg 240
Hominidae; Homo. Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Bruemmendorf, T., Kinnemann, H., Roepcke, S., Hermann, K.,	Qy         241 AlaLysLeuGluGluGluGlnAlaglnGlnIleArgLeuGlnAlagheGlnAlaArg 260           Db         835 GCCAAGCAGGAGCAGCAGAGATACGCCTGCAGGCCTTCCAGGCCCGC 894
Xinzhong, L., Pilarsky, C. and Staub, E. Human nucleic acid sequences obtained from prostatic carcinomas Patent: WO 2004076614-A 100 - SEP-2004; Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);	Qy         261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
<pre>pecht, Thomas (DE); Schmitt, Armin (DE) Location/Qualifiers 11156 /organiam="Homo sapiens" /mol tronge:"assigned DNA"</pre>	Oy 281 GluLygvalGlnAlaAlaValGl7ThrSerAlaAlaProValProSerAspAgnHis 299
/db_xref="taxon:9606"	RESULT 8
Alignment Scores: 1.09e-120 Length: 1156 Score: 1493.00 Matches: 299 Percent Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.0% Mismatches: 0	LOCUS LOCUS LOCUS LOCUS CQ53896 DEFINITION Sequence 19 from Patent WO2004104224. ACCESSION CQ963896.1 GI:56562665 KEYWORDS SOURCE Homo sapiens (human)
100.0% Indels: 2 Gaps: -299) x CQ896276 (1-1156)	M Homo sapiens Eukaryota; Me Mammalia; Eut Hominidae; Ho
1 LygvalGluGlnalavalGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20 	REFERENCE 1 AUTHONS Wright, M.B. TILLE Markers for lxr activation JOURNAL Patent: WO 2004104224-A 19.02-DEC-2004;
21 GINSerGlyGlnArgTrpGlubeuAlabeuGlyArgPheTrpAspTyrLeuArgTrpVal 40 	FEATURES Location/Qualifier  Source   1.1156
41 GInThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60 	/mol_cype_unassigned one /db_xref="taxon:9606" ORIGIN
ArgalaLeumetaspGluThrmetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu	1.09e-120 1493.00 100.0%
81 GINLEUThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100 	: 100.0% Mismaccnes: 100.0% Indels: 2 Gaps:
	-09-827-854A-2 (1-299) x CQ963896 (1-1156) 1 Ly8ValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140 	Db 115 AAGGTGGAGCGGTGGAGACCGGAGCCGGAGCTGCGCCCAGCAGCAGAGTGG 174  Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40

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                         LeuArgLysLeuArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
                                         CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGA
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1007 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
Location/Qualifiers
                                                                                                          GTGTACCAGGCCGGGGCGCGGGGGCGCGGGGGCGCTCAGCGCCATCCGCGAGCGC
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1 (Dases 1 to 1156)
1 (Dases 1 to 1156)
2 Ishida, B., Kern, J., Duncan, K., Bailey, C. and Schwartz, D.M.

Treatments for Age Related-Macular Degeneration
Datent: JP 2005511713-A 1 28-APR-2005,
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
OS Human OF THE UNIVERSITY OF CALIFORNIA
PD 28-APR-2005
PP 06-DEC-2002 JP 2003550736
PR 03-OCT-2002 US 60/415864,07-DEC-2001 US 60/340498 PI brian ishida, john kern, keith duncan, cathy bailey, daniel m PI CC KH Key
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 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCCAGGTCACCAGGAACTG
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                                                                  Treatments for Age Related-Macular Dogeneration.
DD166083.1 GI:83962539
JP 2005511713-A/1.
Homo sapiens (human)
Bilbaura
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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And 1919. Be located on chromosome 19 --Jackson, Bruns and Breslow, PNAS USA 81, 2945-2949 (1984) -- and is believed to be linked to the Apo C-II gene (see separate entry).

The two mutations causing type III hyperlipoproteinemia (apolipoprotein E phenotype E3/3) produces substitutions of Arg for Cys at amino acid II2 and Cys for Arg at amino acid position 142.

Draft entry and printed copy of sequence for [1] kindly provided by L.L. Gill, University of Aberdeen.

Complete source information:

Human liver [1], [J. Biol. Chem. 258, 11422-11422 (1983)], [2], [3], [4] and blood [5], cDNA to mRNA.
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/ product = 'preapolipoprotein E"
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see the separate entry.
[J. Biol. Chem. 258, 11422-11422 (1983)] is too extensively revised relative to [1] to record the revisions in the FEATURES table. The sequence below is that of [J. Biol. Chem. 258, 11422-11422 (1983)] and [3].
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/db_xref="taxon:9606"
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/gene="APOE"
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                                                                                                      ниманувз 1156 bp mRNA linear PRI 21-OCT-2002
Homo sapiens preapolipoprotein E (APOE) mRNA, complete cds.
K00396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human apolipoprotein E mRNA. cDNA cloning and nucleotide sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (bases 577 to 624) (dill.L.L., Peoples.O.P., Pearston,D.H., Robertson,F.W., Humbhries,S.E., Cumming,A.M. and Hardman,N. Isolation and characterisation of a variant allele of the gene for human apolipoprotein E
                                                                                                                                                                                                                                                       apolipoprocein, apolipoprotein E; lipoprotein; polymorphism; very
low density lipoprotein.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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1 (bases 355 to 1156)

1 (bases 355 to 1156)

1 (bases 1.L., McPherson, J., Nussbaum, A.L., Williams, H.W.,

Lofquist-Kahl, F., Karathanasis, S.K. and Zannis, V.I.

Identification and DNA sequence of a human apolipoprotein E cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthesis, intracellular processing, and signal peptide of human
   GAGAAGGTGCAGGCTGCCGTGGGCACCAGCGCCCCCTGTGCCCCAGCGACAATCAC 1011
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    corrected in [J. Biol. Chem. 258, 11422-11422 (1983)], [J. Biol. Chem. 258, 11422-11422 (1983)] correction of [1]. [4] epsilon-3 and variant.
    epsilon-2 allele.

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Rall,S.C. Jr., Newhouse,Y.M., Clarke,H.R., Weisgraber,K.H.,
McCarthy,B.J., Mahley,R.W. and Bersot,T.P.
Type III hyperlipoproteinemia associated with apolipoprotein E
phenotype E3/3. Structure and genetics of an apolipoprotein E3
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The isolation of cDNA clones for human apolipoprotein E and the detection of apoE RNA in hepatic and extra-hepatic tissues EMBO J. 2 (12), 2369-2373 (1983)
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J. Biol. Chem. 259 (10), 6498-6504 (1984)
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594

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Mammalia, Euthoria; Edarchoncoglifes; Frimates; Catafrini; Hominidae; Homo.

28 Straubsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownsteain, M.J., Usdin, F., Casavant, T.L., Scheiver, T.E., Scheetz, T.E., Brownsteain, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boufsand, M.C., Rodrigues, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnetz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC003557 1186 bp mRNA linear PRI 29-JUN-2004
Homo sapiens apolipoprotein E, mRNA (cDNA clone MGC:1571
IMAGE:3355712), complete cds.
BC003557.1 GI:13097698
                                                                                                                                                                                                                                                                                           774
                                                                                                                              180
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
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                                                                                                                                ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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and [4] variant; a in [4]'normal'"
/citation=[4]
/replace="a"
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                      note="in type III hyperlipoproteinemia"
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Mismatches:
Indels:
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/citation=[3]
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/citation=[6]
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Kaser, M.R.
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.Dc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petresecu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Marranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: h Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557324.

Location/Qualifiers
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                                                        Mammalian
                                     Direct Submission
Submitted (20-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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PAT 08-OCT-2004 Genes expressed in treated human C3A liver cell cultures Patent: US 6727066-A 246 27-APR-2004; Incyte Corporation; Palo Alto, CA linear AUTHORS TITLE JOURNAL

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Human, antilipaemic, neuroprotective, nootropic; genetic variant, APOE, apolipoprotein E, haplotyping, familial dysbetalipoproteinaemia; therapy, genotyping, type III hyperlipoproteinaemia; Alzheimer's disease; SNP, atherosclerosis, single nucleotide polymorphism; chromosome 19q13.2; ss.
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                                                                               Sequence:
                                                                                                                                                                                                                                                                                Database
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Gene #224 Human apo

Human

Ab165450 I Abk64514 I Abn95746 C Acc84921 I

/\*tag= b /standard\_name= "Single nucleotide polymorphism (SNP)"

"Human APOE protein"

Result No.

354

414

160

180

594

200

280

834

774

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GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGTGCAGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCGGC
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                                                                                                                                                                           235 AGGGCGCTGATGGACGAGGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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                     41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
                                                                                                                                             ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGGCCGCCTGGTGCAGTACCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses novel genetic variants of human apolipoprotein E (APOE) gene. The invention also relates to compositions and methods for haplotyping and/or genotyphing the APOE gene. The haplotyping methods of the invention are useful for improving the efficacy and reliability of several steps in the discovery and development of drugs for treating disceases associated with APOE activity, e.g. familial.

C adent for treating a specific condition or disease predicted to be associated with APOE activity and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with APOE activity. Genotyping or haplotyping methods are useful to screen for compounds targeting APOE to treat a specific condition or disease predicted to be associated with APOE activity. Genotyping or haplotyping methods are useful to screen for compounds targeting APOE to treat a specific condition or disease associated with APOE activity. The present sequence condition or disease associated with APOE activity. The present sequence is a cDNA encoding human APOE protein. APOE gene is located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genotyping human apolipoprotein gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of gene.
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                                                                                                                                                "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                             "Single nucleotide polymorphism (SNP)"
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                                                            "Single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                                                         nucleotide polymorphism (SNP)
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                                                                                    replace (388, C)
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P-PSDB; AAE15158.
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Best Local Similarity:
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ò 용 ò us-09-827-854a-2.p2n.rng

200 654 220 714 240 774 260 834 280

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The encoded protein is used to treat subjects who are deficient in apolipoprotein-E (or who produce abnormal forms of this molecule) and therefore are likely to suffer from hyperlipidemia, resulting in arteriosclerosis. It can also be used to raise antisera for detecting the protein deficiency or production of abnormal forms. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                           GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                                                                                                                                                                                                                                                                                                                                                          AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
               LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                 CTGGGGCCCCTGGTGGAACAGGGCCGCGTGCGGCCGCCACTGTGGGCTCCCTGGCCGGC
                                                                               GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                  MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                                                                                                                         LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal
                                                                                                                                                                                                                                                                                                            CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCCAGTGGGCCGGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequence coding for human apolipoprotein-E - and expression vectors and transformed cells contg. it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1110 BP; 198 A; 354 C; 415 G; 143 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
15. .968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 2; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human apolipoprotein-E.
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01-JAN-1980
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of covarian tumour marker genes (ABA83181-ABA83182, ABA83180, ABA83181, ABA83181-ABA83181-ABA83181-ABA83181-ABA83181-ABA83181-ABA83181-Or SEGMENTS thereof (ABA83183-ABA83189, ABA83189, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring a patient in remission from ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline serous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified to overexpressed in a broad variety of ovarian epithelial tumour cells contained in mmune response pathways, in the regulation of cell in minume response pathways, in the regulation of cell conjiferation and in protein folding, and many of these are membrane-contained and protein folding, and many of these are membrane-contained and the overexpressed of madition to their uses as diagnosite, and the protein the present and the protein folding to their uses as the protein the protein folding to their uses as a fadagnosite, and the protein the present and the present Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenoma; borderline mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; endifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; denofibroma; Bernner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; ds. Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180, ABA83182 and ABA83184 represent the ovarian tumour marker genes of the Hough CD; Pizer ES, (USSH ) US DEPT HEALTH & HUMAN SERVICES 23; Page 105-106; 140pp; English. Sherman-Baust CA, 03-APR-2001; 2001WO-US010947 03-APR-2000; 2000US-0194336P WPI; 2001-626450/72. P-PSDB; ABB50287 WO200175177-A2 Homo sapiens. 11-OCT-2001 Morin PJ, invention Claim 

G; 147 T; 0 U; 0 Other; Sequence 1147 BP; 210 A; 365 C; 425

Alignment Scores:

ABA83113 standard; DNA; 1147 BP.

ABA83113 ID ABA6 XX

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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (See SEQ ID NO:1 to 4622); (b) the full-inagh coding region of sequence (See SEQ ID NO:1 to 4622); (b) the full-inagh coding region of sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above corporation of moreic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by the full-comprising the above polypeptide; (b) an amino acid sequence encoded by the full-comprising at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) a chimeric polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) a tumour-associated antigonic target (TAT) a process composition of matter comprising the above polypeptide; (10) a composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of the growth of the call is at least in part dependent upon a growth by the call is at least in part dependent upon a growth of the call is at least in part dependent upon a growth of the call is at least in part dependent upon a growth of the call is at least in part dependent upon a growth of the above protein; (13) a method of containing the growth of the call is at least in part dependent upon a growth of the call is at least in part dependent upon a growth of a protein in a sample suspected of containing the proversing of the captured of a protein in a sample suspected of containing the above protein; (16) a method for treating or a protein disorder associated with increased expresses the above protein; and (17) a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reventing or treating cancer. The composition is also used for preparing medicament for the therapeutic treatment or diagnostic detection of a sll proliferative disorder or cancer. The present sequence represents a
                                                                                                                          TAT; cytostatic; gene therapy;
                                                                                tumour-associated antigenic target (TAT) cDNA sequence #3836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy. The composition and methods are useful for diagnosing,
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                                                                                                                        human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 3836; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2002; 2002US-0418988P.
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Sequence 1154 BP; 208 A; 367 C; 431 G; 148 T; 0 U; 0 Other;

ADQ86961 standard; cDNA; 1154 BP

ADQ86961 ID ADQ6 XX RESULT 5

ApoE3

"Human

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apoE humanized mammalian cell useful for screening for agents useful treating or preventing Alzheimer's disease and arteriosclerosis.
                                                            Human; ApoE3; Alzheimer's disease; arteriosclerosis;
                                                                                                                                                                                                                                                                                               Disclosure; Page 13-14; 22pp; Japanese.
                                                                                                  ocation/Qualifiers
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                                            Human ApoE3 coding sequence
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120 100 The present invention relates to an ApoE humanised mammalian cell. The present sequence is the coding sequence for human ApoE3, which was used in the metchod of the present invention. The ApoE humanised mammalian cell can be used for screening for agents useful for treating or preventing Alzheimer's disease and arteriosclerosis 294 174 234 354 9 80 40 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal CAGAGCGGCCACCGCTGGGAACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu CAGACACTGTCTGAGCAGGAGGAGGAGGAGCTGCTCCAGCTCCCAGGTCACCCAGGAACTG GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly U; 0 Other; 1156 299 0 0 0 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                                                                                                                                                                                        MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                                                                                                                                                                        AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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                                     GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC
                                                        LeuArgLysLeuLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla
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                                                                                                                                  CTGGGGCCCCTGGTGGAAACAGGGCCGCGTGCGGCCGCCACTGTGGGCTCCCTGGCCGC
                                                                                                                                                        GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                                                                                   ATGGGCAGCCGGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC
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The invention comprises methods of detecting the presence or absence of at least one allelic variant of a polymorphic region of a gene associated with cardiovascular disease. The invention specifically relates to detecting the region of a cytochrome C oxidase subunit VID (COX6B) gene that is associated with high serum cholesterol, or the region of the Neacetylglucosaminy! transferase component glycosylphosphatidylinositol-1 (GPI-1) gene that is associated with low serum high density lipoprotein (HDL). The methods of the invention are useful for detecting a predisposition to high serum cholesterol, low serum HDL and readiovascular disease. The methods are also useful for elucidating pathological pathways, developing diagnostic assays and new drug theraples for such disorders. The present DNA sequence represents a human cardiovascular disease
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Best Local Similarity:
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The present sequence is a human apolipoprotein E (apoE) isoprotein, apoE3 DNA. The apoE lipoproteins are useful for lowering cholesterol, delaying the onset of atherosclerosis, treating or regressing atherosclerosis without inducing hypertriglyceridaemia, in a mammal lacking an endogenous, normally functioning apoE gene or low density lipoprotein (LDL) receptor or is at risk for developing atherosclerosis due to accumulation of lipoprotein remnants in the bloodstream or having a defect in remnant removal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 354
                    New apolipoprotein E polypeptide and nucleic acid, useful for lowering cholesterol, delaying the onset of or treating atherosclerosis in mammal, without inducing hypertriglyceridemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
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                                                                       Claim 14; Page 81; 91pp; English
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                                              ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
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115. 1011
/product= "Mature human apoE isoprotein, apoE3"
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/*tag= a
/product= "Human apoE isoprotein, apoE3"
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04-OCT-2000; 2000US-00679088
05-APR-2001; 2001US-00827854.
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The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangilosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAS) nucleotide inserted into a virus, a mammalian T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producin (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which
                                                                                                                                                                                                                        GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                   GCCAAGCTGGAGGAGGAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC
                                                                                                                                                LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal
                                                                                                                                                                     MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
                                                                          AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidally performed immunocytes to the host), producing a tumouricidally activated in which receptors for the tumouricidally activated oppulation, and administering APCs to the host), producing a tumouricidal T cell contact T cells, in which adaptor proteins, which inhibit T cell contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally administering the tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells to the host, treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo, producing (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activated) and producing (M7) at edleted or functionally deactivated) and producing (M7) at tumouricidal T cell population in vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contect immunocytes in vivo. The treceptors, methods and compositions are useful for treating cancers and tumouricidal T cell superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motific. The present the contact immunocytes in vivo. The coeptors, methods and compositions are useful for treating cancers and tumours bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins which in the present contact immunocytes in vivo in the present contact in the present co incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patnet office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551" 

Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	Scol	res: arity: nilarity:	1.13e-106 1403.00 100.0% 100.0% 100.0%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1156 299 0 0 0
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δ	7	Lysvalglu	GlnAlaValGluThrGluE	luProGluProGluL	1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp
Db	115	AAGGTGGAG		AGCCGGAGCCCGAGC	
λŏ	21	GlnSerGly	GlnArgTrpGluLeuA	laLeuGlyArgPheT	21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal
Db	175	CAGAGCGGC	CAGCGCTGGGAACTGG	CACTGGGTCGCTTTT	CAGAGCGGCCAGCGCTGGGAACTGGCACTGGCTTTTGGGATTACCTGCGCTGGGTG
<i>ا</i> م	41		SerGluGlnValGlnG	luGluLeuLeuSerS	GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu
qa	235			AGGAGCTGCTCAGCT	CAGACACTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG
λŏ	61	ArgalaLeul	MetAspGluThrMetLy	/sGluLeuLysAlaT	61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
qa	295		ATGGACGAGACCATGA	AGGAGTTGAAGGCCT	AGGCCCTGATGGACGACCATGAAGGACTTGAAGGCCTACAAATCGGAACTGGAAAA
٥٨	81	GlnLeuThr	ProValAlaGluGluT	rArgAlaArgLeuS	81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLygGluLeuGlnAlaAla

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GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly

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GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis

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GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
                                                                                                                                                                                                                                                                                                                                                                           presence or absence of multiple haplotypic genetic variations in a preselected region of one chromosome of a chromosome pair. The method is also useful for determining the linkage phase between two adjacent loci. The method is fast, inexpensive and provides uncomplicated determination of haplotypes in nucleic acid fragments of varying length from 25-40000 base pairs. The present sequence represents the human apolipoprotein E (apoB) coding region nucleotide sequence, which is used in the exemplification of the present invention. Human apoE is located on specification, but the coding sequence of apoE is referred to in Example 3 by Genbank accession number K00396
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multiple haplotypic genetic variation; polymorphism; chromosome 19q13.2;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
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    CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
                                                          GTGTACCAGGCCGGGGGCGCGCGCGCGCGCGCCTCAGCGCCTTTGCAGCGCCATCCGCGAGCGC
                                                                                              LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                                                                                                   CTGGGCCCCTGGTGGAACAGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGC
                                                                                                                                                           GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
                                                                                                                                                                                                                                                      AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
                                   ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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                                                                                                                                                                                                                                                                                                                                 Nuclear hormone receptor ligand; ophthalmological; cholesterol transport; lipid efflux; macular degeneration; apolipoprotein E; apo E; human; gene;
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                                                                                                                                        GluLygValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                                                             LeuLysSerTrpPheGluProLeuValGluAspWetGlnArgGlnTrpAlaGlyLeuVal
                 CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholesterol transport in an ocular tissue and involves delivering at least one nuclear hormone receptor ligand. The method is used for increasing lipid efflux and reverse cholesterol transport in ocular tissue, preferably retinal pigment epithelium (RPE) and/or Bruch's membrane, in an individual afflicted with AMD or Stargardts disease (fundus flavimaculatus), and for treating macular degeneration. The present sequence represents a DNA encoding a human apolipoprotein E (GenBank Accession No. K00396)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (MI) for identifying a nucleic acid by means of fluorescence resonance energy transfer (FRET). MI comprises: (a) providing a first nucleic acid containing the nucleotide to be identified in a single-stranded containing the nucleotide to be identified in a single-stranded of identified and the aequence immediately in 3' to the nucleotide to be complementary to the sequence of the first nucleic acid immediately in 3' to mucleotide to be identified, and a first FRET-generating to the nucleotide to be identified, and a first FRET-generating in a nucleic acid, where the sequence immediately in 3' to the nucleotide for the inverpohere linked to a nucleotide from 1-12 nucleotides far apart from the 3' terminal nucleotide of the second nucleic acid; (c) hybridising the first and second nucleic acid, resulting in a nucleic cod, bybridising the first and second nucleic acid, resulting in a nucleic cod, bybridising the first and second nucleic acid, polymerase and locotide chemically linked to a second FRET-generating couple stranded conformation, of the first nucleic acid polymerase to parform a single base extension at the 3' end of the first nucleic acid, and (f) has extension at the 3' end of the first nucleic acid, and (f) the nucleotide chemically linked to the second FRET-generating fluorophore conclude chemically linked to the second FRET-generating fluorophore conclude chemically linked to the second FRET-generating the nucleic acid polymerases for the same nucleotide when labelled or non-labelled by employing MI; (4) sequencing nucleic acid above, comprising at the present anucleic acid above, comprising at the midelide fluore and kill for the methods described above, comprising a and kits of the present invention are useful for identifying a SMP or mucleic acid by employing MI; (4) sequencing nucleic acid polymerases or the preference of nucleotide flow aparting the extension of properties of nucleotide second FRET-generating fluorophore polymerases or the preference of 
                                                                                            identification; fluorescence resonance energy transfer; FRET; single nucleotide polymorphism; SNP; mutation; nucleic acid polymerase; nucleic acid sequencing; human; apolipoprotein B; ApoE; chromosome 19q10.2; gene; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a nucleotide in a nucleic acid by means of Fluorescence Resonance Energy Transfer by monitoring the presence or absence of incorporation of the nucleotide chemically linked to the second FRBT-
                                                Human apolipoprotein E (ApoE) encoding cDNA SEQ ID NO:1.
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encodes human apolipoprotein E (ApoE), which
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         sequence encodes human apolipoprotein E (A) le from the present invention. Human ApoE
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                                        295 AGGCGCTGATGGACGAGGACCATGAAGGCCTTGAAGGCCTACAAATCGGAACTGGAGGAA
                                                                                                          CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGCTGTCCAAGGAGCTGCAGGCGGCG
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                                                                                                                                                                                                                   receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; apolipoprotein; ds.
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                                                                                                                                                                                                                                                                           The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological cresponse. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the invention of an immunopathological condition in a sample, conditions to form one or more hybridisation complexes, detecting the conditions to form one or more hybridisation complexes and comparing the levels of the detected to hybridisation complexes with the level of hybridisation complexes with the level of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and comparing the expression of target polymucleotide probes. The converse are useful as hybridisable array elements in a microarray for monitoring the expression of target polymucleotides. The microarray for monitoring the expression of target polymucleotides. The microarray for monitoring culcarative colitis, hyperecesinophila, irritable bowel syndrome, culcarative colitis, hyperecesinophila, irritable bowel syndrome, carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenicity studies, forensics or pharmacogenomics. The composition carcinogenic fragments. This sequence captresents a human cDNA of the invention. Note: The sequence data for this patent did not form part of fram intent promo at secdinar and the leader of the primed specification of the prime of the prime of the primed specification of the prime of the primed specification of the prime of the composition of the prime of
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                                                                                                                                                  A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGTGGAGCAAGCGGAGACAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGG
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                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1007; SOpp; English.
                                                                            Seilhamer JJ;
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P-PSDB; AEB86466.

Marker for screening for compounds influencing a gene or protein, for treating cartilage disorders, such as, osteoarthritis, comprises a polynucleotide or a complement to specific genes, or an antibody to its protein.

Claim 1; SEQ ID NO 13; 64pp; Japanese.

The invention relates to a novel marker for cartilage disorders. The marker consists of a polymucleotide sequence of 15 bases from the sequence of acetyl-conzyme A acetyltransferase 1, Rev-Erbh-beta, Selenoprotein P, aquaporin 1, BMP-1b; FK506-binding protein 1A, apolipoprotein B, acyl-coA synthetase 5, epoxide hydrolase 1, or consists of lithese gene, and/or a polymucleotide complementary to one of these. The invention further comprises: a detection method of a cartilage disorder; a disease marker for cartilage disease containing an antibody control acid, as given in the specification; a detection method of a cartilage disorder using a protein sample from the subject, or a peptide from it, and the antibody as a label; screening for a material which controls expression of one of the genes above; screening for a material which which controls the activity or function of one of the proteins; and an agent to improve or treat a cartilage disorder which contains a substance controlling expression of the genes or activity of the proteins. The markers may be used as a probe or a primer, for diagnosis of conditions such as esteoarthritis, chordrodystrophy, discopathy, cartilage damage, semilunar cartilage disorder, deficient healing of fractures, or in chondrocyte transplants. The screening methods are useful for identifying therapeutic compounds. This polymuclectie sequence represents the DNA encoding apolipoprotein E of the invention. 

Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 1.13e-106 1493.00 100.0% 100.0% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match:

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US-09-827-854A-2 (1-299) x AEB86465 (1-1156)

1 LysvalglucinalavalgluthrcluProcluProcluLeuargclucinthrcluTrp 20 	GinserGlyglnargTrpGluLeualaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40 	GlnThrLeuSerGluGlnValGluGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60 	ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80 	GInteuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100 	GInAlaArgLeuGlyAlaAspNetGluAspValCysGlyArgLeuValGlnTyrArgGly 120 	GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140 	141 LeuArgiysLeuArgiysArgieuLeuArgAspAlaAspAspLeuGlniysArgieuAla 160
LysValGluGlnAla 	GinserGlyGlnArg	GlnThrLeuSerGlı 	ArgAlaLeuMetAsp 	GlnteuThrProva.	Glnalaargreugl; 	GluvalGlnAlaMel 	LeuArgLysLeuArg
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qq	535	
ò	161	ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
qq	595	GTGTACCAGGCCCGGGGCCCGCGGCGCCCGAGCGCGCCCTCAGCCCCATCCGCGGCGCC 654
λ̈́δ	181	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Dp	655	CTGGGGCCCCTGGTGGGTGTGTGTGTGTGTGTGTGTGTG
δλ	201	GInProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
QQ	715	CAGCCGCTACAGAGAGCGGGCCCAGGCCTGGGCGAGCGCTGCCGCGCGCG
ò	221	MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
qq	775	ATGGGCAGCCGGACCCGCACCGCCTGGACGAGGTGAGCAGCTGGCGGGGGGGG
ò	241	AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Dp	835	GCCAAGCTGGAGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894
ò	261	LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Dp	895	CTCAAGAGCTGGTTCGAGCCCCTGGTGGAAGACATGCAGCGCCAGTGGGCCGGGCTGGTG 954
ά	281	GluLysvalGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
ф	955	GAGAAGGTGCAGCTGCGTGGGCACCAGCGCCCCCTGTTGTTTTTTTT
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Job time : 1035.05 secs

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UI-E-EJO-602287404 602649975

602513830

OM protein

6

Sequence:

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Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 975)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
                                                                                                                                                                                                      BL600563 60324936
BCC44785 Mus muscu
AK139517 Mus muscu
AK139517 Mus muscu
AK139105 Mus muscu
AK149568 Mus muscu
AK149568 Mus muscu
AK159424 Mus muscu
BGB29472 60273768
BU194461 AGENCOURT
DN102220 1097106 M
BF967857 60228176
AK150834 Mus muscu
BF967857 60228176
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ILLUMIGEN MCQ 48393 Katze MMLV Macaca mulatta cDNA clone
IBIUW:18409 5' similar to Bases 755 to 975 highly similar to human
Unigene H8.515465, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DV789745 HW LIVER
DR772634 ILLUMIGEN
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CA307890 UI-H-FT1-
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BU190668 AGENCOURT
AK131624 Mus muscu
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G707147 602670283
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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VERSION
KEYWORDS
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AUTHORS
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COS80643
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                                                                                                     Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=\dask_ABSSWEB spool/US09827854/runat 14062006 081827 26762/app query.fasta_1
-Q=\dask_ABSSWEB spool/US09827854/runat 14062006 081827 26762/app query.fasta_1
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNIYS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LisT=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXEN=200000000 -HOST=abss02h
-USFR=US0982784 @CGN_1 1 7986 @runat 14062006 081827 26762 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0,5 -FGAPOP=6 -FGAPEXT=7
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Database :

Result . 02

Minimum DB Maximum DB

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CO775017

937 bp mRNA linear EST 04-AUG-2004
ILLUMIGEN MCQ 52207 Katze MNLV Macaca nemestrina cDNA clone
IBIUW.28964 5' similar to Bases 5 to 934 highly similar to human
APOE (Hs.110675), mRNA sequence.
CO775017.1 GI:50976280
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Bmail: cmagness@illumigen.com

Sequenced on 2004.07.21. 706 Q20 bases. Library Preparation: Prof.

Michael Katze Lab at University of Washington DNA Sequencing:

Illumigen Biosciences Inc. For further information, see
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1 (bases 1 to 937)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. an Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human
              LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
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11Unigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134,
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca nemestrina (pig-tailed macaque)
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/strain="Indian"
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 937 Std Brror: 0.00
Plate: CL000549 row: B column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
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/clone_lib="Katze_MNLV"
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PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
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Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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Sequenced on 2004.07.02. 690 Q20 bases. Library Preparation: I Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org
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/tissue_type="hypotalamus"
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: Sall-XhoI (qrcgan; plago-dT primed using primer
5-TTTTTTTTTTTTTTTVVN-3', size_selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHORI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1027)
S NIH-MGC http://mgc.nci.nih.gov/.
In National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: Gapple-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11790 row: 1 column: 09
High quality sequence stop: 845.
Location/Qualifiers
Lrce
1. 1027
                                                 BI670367 1027 bp mRNA linear EST 12-SEP-2001
603292738F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312024 5',
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Conservative:
Mismatches:
Indels:
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80.3%
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Homo sapiens
                                                                                   mRNA sequence.
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/note="Organ: liver; Vector: pDONR 222; Site_1: BsrG
Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="txxxxxxn:9606"

/clone="IMAGE:4860585"

/tissue_type="melanotic melanoma, high MDR (cell line)"

/lab_host="MHH MGC_49"

/clone=lib="NHH MGC_49"

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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN) BNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1718 row: b column: 10
High quality sequence stop: 817.
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// Libaknon:9606"
// Libaknon:brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamH; Site 2: Sall-XhoI pBluescript KS+); Site 2: Sall-XhoI pBluescript KS+); Site 3: Sall-XhoI pBluescript KS+); Site 4: Sall-XhoI pBluescript KS+); Site 5: Sall-XhoI pBluescript KS+); Site 6: Sall-XhoI pBluescript KS+); Site 7: Sall-XhoI pBluescript KS+);
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1. (bases 1 to 933)

2. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

4. Unpublished (1999)

4. Unpublished (1999)

5. Contact: Robert Strausberg, Ph.D.

5. Email: cgapbs-r@mail.nih.gov

7. Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

6. Contact: Robert Strausberg, Ph.D.

7. Esue Procurement: Miklos Palkovits, M.D., Ph.D.

6. Contact: Robert Straved by: The I.M.A.G.E. Consortium (LLNL)

7. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7. DNA Sequencing by: Incyte Genomics, Inc.

7. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

7. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8. Play1.798 row: a column: 21

8. High quality sequence stop: 780.

9. Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:5314844 5',
                                                688
                                                                                               220
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                                                                                                                                                                                           Met-GlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValAr 240
                                                                                            GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaliaia; Eutheria; Buarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

I (bases 1 to 909)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Nutional Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: Gapba-r@mail.nih.gov

Tissue Procurement: Rubin Laboratory

Contact: Robert Strauberg by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2831 row: j column: 09

High quality sequence stop: 574.
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                                                                                     280 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAATCGGAACTGGAGGAA
                                                                                                                                                                                 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly
                                                                                                                                                                                                                                                                                                                                               121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                                                                                                                                                                                                                                                                                                                                             460 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGGTGCGCTCGCCTCCCAC
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AGENCOURT_10440638 NIH_MGC_109 Home sapiens cDNA clone
INAGE:6598569 5', mRNA sequence.
BU849868.1 GI:24034831
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/clone="INAGE:6598569" |
/tissue_type="texatocarcinoma, cell line" |
/lab_host="DH10B (phage-resistant) |
/clone_lib="NIH_MGC_109"
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NIH-MGG http://mgc.nci.nih.gov/.
NIH-MGG http://mgc.nci.nih.gov/.
UURNAL
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OCHICLEC TORIGINE S. Gerhard, Ph.D.
CONCECT: Daniels S. Gerhard, Ph.D.
CONCECT: Daniels S. Gerhard, Ph.D.
CONCECT: Daniels S. Gerhard, NIH
Bldg. JR man,007 Bethemat. M.D. 20892
Email: gapphe refraction: Express Genomics. Inc.
CDNA Library Preparation: Express Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
http://inage.libr.gov
clone distribution: MGC clone distribution information can be
http://inage.libr.gov
clone distribution: MGC clone distribution information can be
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clone distribution: MGC clone distribution information can be
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preparation: Express
Seq primer: JRMRX (CMGAAAGAGCARGACCARGACCA
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 938)
S NIH-MGC http://mgc.nci.nih.gov/.
S National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboration
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin at:
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC column: 12
High quality sequence stop: 767.
Location/Qualifiers
                                                                                                             938 bp mRNA linear EST 15-MAY-2001
Homo sapiens cDNA clone IMAGE:4841411 5',
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  875 GGGCCCGCTTCAAGAACTGGTTCCAGCCC 903
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602717942F1 NIH_MGC_49
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/note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2: Xhoi; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xhoi sites using the following 5' adaptor: GGCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superseript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Bukaryota Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordate; Craniata; Vertebrata; Euteleostomi;

Hominidae; Homo.

1 (bases 1 to 942)

S NIH-McG http://mgc.nci.nih.gov/.

L (bases 1 to 942)

L (brand Institutes of Health, Mammalian Gene Collection (MGC)

L (bround Library Preparation: Michael J Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J Brownstein (LINL)

DNA Sequencing by: The I M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.lln.gov

Plate: LLAMI1762 row: a column: 11

High quality sequence stop: 762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GluValArgAlatysLeuGluGlu-GlnAlaGlnGlnIleArgLeuGlnAla--Glu 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluvalGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                                                                                                                                                   GAGGTGCAGGCCATGGTCGGCCAGAGCACCGAGAGCTGCGGGTGCGCCTCGCCTCCCAC
                                                                                                                                                                                                                                            CTGCGCAAGCTGCGTAAACGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA
                                                                                                                                                                                                                                                                                  ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
                                                                                                                                                                                                                                                                                                    LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySer-LeuAlaGl
                                                                                                                                                                                                                                                                                                                                                         yGlnProLeuGlnGluArgAlaGlnAlaTrp-GlyGluArg-LeuArgAlaArgMetGlu
                                                                                                                                                                                                                                                                                                                                                                                                                          ---GluMetGlySerArgThr-Arg-AspArgLeuAspGluValLys-GluGlnValAla
                                                      GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla
                                                                                   CAACTGACCCCGGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGGTGCAGGCGGCG
                                                                                                                                                                                                                            LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AlapheGinAlaArgLeuLysSerTrppheGluProLeuVal 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    891 GGCTTCCCAGGCCGGCTCAAAAGCTGGTTGAAGCCCTGGTT 932
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234 273 293

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603615713F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420618 5',
BM042094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluGlnValAlaGluValArgAlaLysLeuGluGluGluGlnAlaGlnGlnIleArgLeuGln 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 ACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCCAGGCCTGGGGCGAGCGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTIGCGCGCGCGATGGAGGAGATGGGCAGCCGGACCCGCGACCCCTGGACGAGGTGAAG 294
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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rLysGlu--LeuGlnAlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGly
                                                                                                                                                                                                               713 CAAGGACGCTTGCAGGCGCGCGCAGGCCCGGCTGGGCGGGGACATGGAGGACGTGTGCGGC
                                                                                                                                                                                                                                                                               114 ArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeu
                                                                                                                                                                                                                                                                                                               134 ArgValArgLeuAlaSerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAsp
                                                                               ysSerGluLeuGlu-GluGln-LeuThrProValAlaGluGluThrArgAlaArgLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                 593 CGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGGCTCCTCCGCGATGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspleuGlnLysArgleuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGly
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1 (bases 1 to 800)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DTPDTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/mol_type="mRNA"
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/note="Organ: sKin; Vector: poTB7; Site_1: Site_2: Sit
                                                                                                                                                                                                                                                                                                                                                                                                            BM042676 834 bp mRNA linear EST 07-NOV-2001
603616028T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420598 3',
mRNA sequence.
                                                       239
                                                                                                                                                                                                          905
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Capaba-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: The I.M.A.G.E. Consortium (LLML)

Cone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

Plate: LLCM1875 row: h column: 07

High quality sequence start: 23

High quality sequence stop: 834.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                               220 luMetGlySerArgThrArgAspArgLeuAsp-GluValLys-GluGlnValAlaGluVa
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                          258 lnAlaArgLeuLysSerTrpPheGluPro 267
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97.2%
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Homo sapiens
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56 ValThrGlnGluLeuArgAlaLeuMetAspGluThrMet--LysGluLeuLysAlaTyrL 75

us-09-827-854a-2.p2n.rst

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/tissue_type="retinoblastoma"
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RocRI; cDNA made by oliqo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                            927 bp mRNA linear EST 21-MAR-2001 602513830F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4645759 5', BG472299
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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644 CTGGGGCCCCTGGTGGAACAGGCCGCGTGCGGGCCAGCACTGTGGGCTCCCTGGCCGGC
                                                                              GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu
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1 (bases 1 to 927)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                      MetGlySerArgThrArgAspArgLeuAspGluVal 232
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Matches:
Conservative:
Mismatches:
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/db_xref="taxon:9606"
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91.8%
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Homo sapiens
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Query Match:
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/note="Organ: poTB7; Site 1: XhoI; Site 2: Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AGGGCCCTGATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1875 row: i column: 03
High quality sequence stop: 792.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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/organisme"Homo sapiens"
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
Plate: LLAM11760 row: b column: 04
High quality sequence stop: 782.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                      / Organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db Zref="taxon:9606"
/clone="IMAGE:5300259"
/issue type="hypothalamus"
/lab host="DH10B"
/clone lib="NIH MGC 96"
/note="Torgan: brain; Vector: pB
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1 (bases 1 to 922)

1 Mth-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                           AGGGCGCTGATGGACGAGCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAAA
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BF967543 954 bp mRNA linear EST 23-JAN-2001 602287404T1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4374576 3', mRNA sequence.

BF9667543. GI:12334758
AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Poveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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/dev stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UT-8-20"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
UT-8-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double strand cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonoclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Contact: Soares, MB
Contact: Soares, MB
Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9256
Fax: 319 335 9256
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seq primer: All Reverse.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="UT-E-EXO-aiu-1-08-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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                                                                                                                                                                                                                                                                                                                                                                   846 GGGCCACAAGCTGAAGAAAAAAAAAAAAAAAAAAACGCCTTA---GCCGAAGGCTTCAGG 899
   GluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluVal
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM728696 106 bp mRNA linear EST 01
UI-E-EJO-aiu-l-08-0-UI.rl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-aiu-l-08-0-UI 5', mRNA sequence.
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/clone="Indexcolling"
/lisue type="hypothalamus"
/lab_host="Untlob"
/clone lib="NIH MGC 96"
/clone lib="Organ: brain; Vector: pBluescriptR (modified pBluescript K3+); Site_l: BamHl; Site_2: Sall-XhoI
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/crcgag); Oligo-dT primed using primer
/crcgag); Oligo-dT primed using primer
/crcgag); Oligo-dT primed using primer
/crcgag; Si & a normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein
(NIHH/MHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10038 row: h column: 01
High quality sequence start: 16
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 954)
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                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGGTATCAGGCC
                                                                                                                                                    ThrargaspargleuaspGluValLysGluGlnValAlaGluValArgAlaLysLeuGlu
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Sequence 1007, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Guean G. Stuart
APPLICANT: Gueffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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MEDIUM TYPE: Floppy disk
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COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
US-10-211-689-31

US-10-211-689-31

US-10-211-689-43

US-10-211-689-43

US-08-949-115-51

US-09-819-964-51

US-09-819-964-51

US-09-819-964-51

US-09-810-107-2491

US-09-11-689-39

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US-09-818-875-3404

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ATTORNEY/AGENT INFORMATION:
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CITY: PA
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Sequence 1, Appli
Sequence 2244, Ap
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 37, Appli
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FEMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
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                                                                                                                                   June 14, 2006, 19:03:31 ; Search time 312.205 Seconds
    GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-919-039-246
US-07-709-949-1
US-09-880-107-2244
US-09-108-006C-3
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APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT APPLICATION NUMBER: US/09/919,039

PRIOR PAPLICATION NUMBER: 60/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

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LENGTH: 1291
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                            AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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OTHER INFORMATION: Incyte ID No. 6727066 2514988CB1
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Matches:
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                                                                                                                                                                                                                          ; Sequence 246, Application US/09919039; Patent No. 6727066; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
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COTHER INFORMATION:
US-09-919-039-246
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NAME/KEY: unsure
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US-09-919-039-246
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Matches:
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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1493.00
100.0%
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; CLONE: 9178850
US-09-023-655-1007
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Best Local Similarity:
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                             LENGTH: 1157 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRN
                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc signal
LOCATION: 62.119
PUBLICATION INFORMATION:
AUTHORS: McLean, J W
JOURNAL: 259urnal of Bic
   FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Query Match:
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                             121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                                                      LeuhrgLysLeuhrgLyshrgLeuleuhrghsphlahsphspLeuGlnLyshrgLeuhla
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                                                 600 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/709,949
FILING DATE: 19910604
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFRENCE/DOCKET NUMBER: 9629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
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STREET: P.O. Box 2113
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CITY: Madison
STATE: WI
COUNTRY: USA
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US-07-709-949-1
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McLean, J W
Journal of Biological Chemistry
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Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
CORRESPONDENCES: 62
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
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APPLICATION NUMBER: US/09/108,006C
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CITY: Newtown
STATE: PA
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APPLICANT: Steer, Clifford J. Kren, Betsy T.
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OTHER INFORMATION: Genbank Accession No. 6974667 M12529
US-09-880-107-2244
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 2244, Application US/09880107
; Patent No. 6974667;
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Scherk, Uwe
; APPLICANT: Scherk, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in 1
; FILE REFERENCE: 4921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR PILING DATE: 2000-06-14
; PRIOR PILING DATE: 2000-06-14
; PRIOR PILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 2244
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3805
298
0
1
195
195
FILING DATE: 30-Jun-1992
CLASSIFCATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: 60/074,497
FILING DATE: 30-APR-1998
ATTORNEY/AGRNT INFORMATION:
NAME: Friebel, Thomas
REGISTRATION NUMBER: 2926
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELEFRANKINGATION: 18FORMATION:
TELEFRANKINGATION INFORMATION:
TELEFRANKINGATION INFORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 71...114
OTHER INFORMATION: Exon 1
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                         TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3805 base pairs
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
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1363.50
60.4%
60.4%
91.3%
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Best Local Similarity:
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Pred. No.:
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TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal 283
                              ProvalAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAlaGlnAlaArg 103
                                                                                              104 LeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
                                                                                                                    164 AlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyPro 183
                                                                                                                                                                                                                                                                                                                                                         LeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeu 203
                                                                                                                                                                                                                                                                                                                                                                                                                         204 GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeu 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlugluglnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer 263
291 ATAGAGGAGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGGTGGAGGCGCAGCTGGGC 350
                                                      LeuargiysargLeuLeuargaspalaaspaspleuGlniysargLeualaValTyrGln
                                                                                                                                                                                                                                                                                                             124 AlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Piedrahita, Jorge A
APPLICANT: Piedrahita W
TITLE OF INVENTION: Compositions and Methods for the
Generation of Transgenic Animal Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLD, WHITE AND DURKEE STREET: P.O. Box 4433
CITY: Houston STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/819,964
FILING DATE: 28-Mar-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09819964; Patent No. 6369294; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GluThrGluProGluProGluLeuArg-----GlnGlnThrGluTrpGlnSerGly 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu
                                                                 APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1126
212
40
40
4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                            STREET: P.O. BOX 4433
CITY: HOUSTON
                  Sequence 5, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
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1082.00
85.1%
71.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51..1001
                                                                                                                                                                                               CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
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Best Local Similarity:
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US-08-949-155-5
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Pred. No.:
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      US-08-949-155-5
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us-09-827-854a-2.p2n.rni

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APPLICANT: Rieger, Daniel K.
APPLICANT: Rieger, Daniel K.
APPLICANT: Simimkets, Richard A.
APPLICANT: Simimkets, Richard A.
APPLICANT: Simimkets, Richard A.
APPLICANT: Simithson, Glennda
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spote Edward Z.
APPLICANT: Shong Med
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC
FILE REPERBACE: 21402-4168
FRICH APPLICATION NUMBER: 60/311751
PRIOR PILING DATE: 2001-00-10
PRIOR PILING DATE: 2001-00-10
PRIOR PILING DATE: 2001-00-00
PRIOR PILING DATE: 2002-02-15
PRIOR PILING DATE: 2001-00-10
PRIOR PILING DATE: 2002-04-15
PRIOR PILING DATE: 2001-00-13
PRIOR PILING DATE: 2001-00-13
PRIOR PILING DATE: 2002-05-15
PRIOR PILING DATE: 2001-00-13
                                                                                                                                                                                              GluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer 263
                                                                                                                                                                                                                                                                                                                             891 TGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGGCCGGGCTGGTGGAGAGGATG 950
                                                                                                                             771 CGGACCCGCGACCGCCTGGATGAGATGCGTGAGCAGCTGGAGGAGGAGGAGGCGCCCAAAGTG
                            ArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeu
                                                                                                                                                                                                                          TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal
  GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                 284 GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn 298
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/10211689 Patent No. 6974684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Algobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Grow, Xiaojia (Sasha)
APPLICANT: Khramstov, Nikolai V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peyman, John A.
Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
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US-10-211-689-37
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuGlyAlaAspWetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGln 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCGCAAGCGGCTGCTCCGCGACACCGAGGACCTGCAGAAGCGCCTGTGCTACCAG 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeu 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAlaValTyrGln 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 MetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGluGlnLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluThrGluProGluProGluLeuArg-----GlnGlnThrGluTrpGlnSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
       FILING DATE: «Unknown»

PILING DATE: «Unknown»

PILING DATE: «Unknown»

PILING DATE: «Us 60/046,094

RIGHER OS-MAY-1997

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: 7AMK:177

TELECOMMUNICATION INFORMATION:

TELEPRAM: (713) 789-2679

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1126 base pairs

TYPE: nucleic acid

STAFE: nucleic acid

STAFE: nucleic acid

STAFE: nucleic acid
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APPLICATION NUMBER: 08/949,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 51..1001
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.04e-95
1082.00
85.1%
71.6%
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Best Local Similarity:
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GENERAL INTORMATION.

APPLICANT: Aldebrook, John II

APPLICANT: Aldebrook, John II

APPLICANT: Aldebrook, Genterine E.

APPLICANT: Burges (Getherine E.

APPLICANT: Burges (Getherine E.

APPLICANT: Gorman, Stacle J.

APPLICANT: Gorman, Stacle J.

APPLICANT: Gorman, Linda

APPLICANT: Gorman, John N.

APPLICANT: Harbory Denies C.

APPLICANT: Harbory Collegial, John R.

APPLICANT: Harbory Collegial, John R.

APPLICANT: Harbory Collegial, John R.

APPLICANT: Gorman, John A.

APPLICANT: Gorman, John A.

APPLICANT: Grand A.

APPLIC
                                                                              GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
718
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US-10-211-689-35
Sequence 35, Application US/10211689
Patent No. 6974684
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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             SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 37
LENGTH: 664
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1026.00
71.6%
71.6%
68.7%
                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                            ) NAME/KEY: CDS
; LOCATION: (2)..(664)
US-10-211-689-37
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Best Local Similarity:
Query Match:
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        Conservative:
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
          71.6$
71.6$
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-211-689-31
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APPLICANT: Shinkets, Richard A. APPLICANT: Spitek, Kimberly A. APPLICANT: Vernet, Corine A. M. TITLE OF INVENTION: THEAAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHON FILES OF INVENTION NUMBER: 06/311/51
RICHER FILING DATE: 2001-08-10
RRICH PLING DATE: 2001-08-10
RRICH PLING DATE: 2001-08-08
RRICH PLING DATE: 2001-08-08
RRICH PLING DATE: 2001-08-08
RRICH PLING DATE: 2001-08-08
RRICH PLING DATE: 2002-02-28
RRICH RILING DATE: 2002-03-28
RRICH RILING DATE: 2002-03-38
RRICH RELING DATE: 2002-03-46
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Patturajan, Meera
Rieger, Daniael K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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US-10-211-689-43
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Query Match:
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LENGTH: 652
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                                                                     101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Boldog, Perenc L.
APPLICANT: Budgess, Catherine B.
APPLICANT: Buggess, Catherine B.
APPLICANT: Gaman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Perman, John R.
APPLICANT: Peyman, John A.
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PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/310,802
PRIOR APPLICATION NUMBER: 60/310,795
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-09
PRIOR PLING DATE: 2001-08-09
PRIOR PLING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/363,050
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-05-15
PRIOR PILING DATE: 2002-05-15
PRIOR PELING DATE: 2002-05-15
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
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PRIOR PILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-09-21
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-211-689-41
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Pred. No.:
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND
FILE REFERENCE: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/311751
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                                                                                                                   GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC
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                                           GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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                      GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly
                                                                                                                                                                                             CTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGAC-----
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Patent No. 6974684
GENERAL INFORMATION:
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APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Hepley, Denise M.
APPLICANT: Hepley, Denise M.
APPLICANT: MacDougall, John R.
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Kimberly A.
APPLICANT: Vors, Kimberly A.
APPLICANT: Vors, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-211-689-41
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PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR PILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR FILING DATE: 2001-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOFTWARE: CLIASSEQLIST VERSION 0.1
ERNOTH: 788
LENGTH: 788
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Matches:
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ORGANISM: Homo sapiens
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, LOCATION: (18)..(704)
US-10-211-689-33
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Best Local Similarity:
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APPLICANT: Pena, John A.
APPLICANT: Peyman, John A.
APPLICANT: Simkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Sytek, Kimberly A.
APPLICANT: Sytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Chong, Mel
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL FILE REPERENCE: 21402-416B
CURRENT APPLICATION NUMBER: 06/311/51
PRIOR APPLICATION NUMBER: 60/311/51
PRIOR APPLICATION NUMBER: 60/310,795
PRIOR PILING DATE: 2001-08-08
PRIOR PELING DATE: 2001-08-08
PRIOR PELING DATE: 2001-08-08
PRIOR PELING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR PILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-15
PRIOR PILING DATE: 2002-02-15
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       161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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                                                                          LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/10211689
Patent No. 6974684
GENERAL INFORMATION
APPLICANT: Alachrock, John II
APPLICANT: Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     duo, Xiaojia (Sasha)
Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
Peturrajan, Meera
Rieger, Daniel K.
Shimkete, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
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Burgess, Catherine E.
Casman, Stacte J.
Edinger, Shlomit R.
Gangolli, Esha A.
Gorman, Linda
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                                                    GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu
                                                                                                                       SerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu-----
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                                                                                                                                                                                                          GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
                                                                                                                   LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal
                                                  241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4267
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APPLICATION NUMBER: US/08/949,155
FILING DATE: CONCURRENTLY Herewith CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ARNOLD, WHITE AND DURKEE STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
STATE: TX
COUNTRY: UX
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 51:
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TYPE: nucleic acid
STRANDEDNESS: single
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                               24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu
                                                                                   SerGluGlnValGluGluGluLeuSerSerGlnValThrGlnGluLeu----
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     GTGCGCACCAAAGTGGAGGAGCAGGCAGCCAGTTGCGCCTGCAGGCCGAGGGATTCCAC
                                                  GCCCTCCTCAAAAGGCTGGTTCGAGCCTCTGGTGGAAGACATACGGCGCCAGTGGGCCGGG
                                                                                    LeuValGluLysValGlnAlaAlaValGly---ThrSerAlaAlaProValProSerAsp
                                AlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGly
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Animal Species
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Transgenic
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/949,155
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,071
REPERENCE/DOCKET NUMBER: TAMK:177
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/819,964
FILING DATE: 28-Mar-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compositions a
                                                                                                                                                                                                                                                                 APPLICANT: Piedrahita, Jorge A
                                                                                                                                                                                                                         Sequence 51, Application US/09819964
Patent No. 6369294
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEFAX: (713) 789-2679
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 77210-4433
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STATE: TX
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Best Local Similarity:
                                                                                                                                                                      3749 AAT 3751
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Sequence 106, App Sequence 106, Appl

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Sequence 5, Appli Sequence 1, Appli

Sequence 246,

Sequence Sequence

Sequence

256, App 8338, Ap

12, Appl 9, Appli

Sequence Sequence Sequence

Title: Perfect score:

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Run on:

Scoring table:

Searched:

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Sequence 11, Appl
Sequence 224, App
Sequence 224, App
Sequence 655, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 1291, App
Sequence 1291, App
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Sequence 1, Appli
Sequence 17, Appl
Sequence 1, Appli
Sequence 1007, Ap
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Sequence 63, Application US/10257021
Sequence 63, Application US/10257021
Sequence 63, Application US/0257021
GENERAL INFORMATION:
APPLICANT: Morin, Patrice J.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTYON: TUMOR MARKERS IN OVARIAN CANCER FILE REFERENCE: 14014.036902
CURRENT FILING DATE: 2002-10-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            US-10-852-335A-10
US-10-937-758A-106
US-10-773-446-63
US-11-186-284-5
US-11-055-309A-1
US-11-059-182-34
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US-11-055-309A-3
         US-09-870-759-129
US-09-802-640-17
US-09-751-708A-129
US-10-301-822-8
US-10-313-641-1
US-10-403-902A-17
US-10-428-551-1
US-10-641-643-1007
US-10-428-817A-125
US-10-428-817A-125
US-10-428-817A-125
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US-10-044-030-454
US-10-10-10-68-08-38
US-09-827-854-12
US-09-827-854-19
US-09-827-854-11
US-09-827-854-11
US-09-827-854-11
US-09-827-854-11
US-09-80-107-2244
US-09-980-107-2244
US-09-960-106-655
US-09-960-106-655
US-09-1313-641-3
US-10-313-641-3
US-10-313-641-3
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US-11-091-883-126
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ORGANISM: Homo sapiens
                                                                                                                                                US-10-257-021-63
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1389.5
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1378
              SEQ ID NO 63
LENGTH: 114
                             Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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-MODEL-frame+ p2n.model -DEV=x1h
-Q=/abss/ABSSWEB spool/US09827854/runat 14062006 081838_26978/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US09827854/runat 14062006 081838_26978/app_query.fasta_1
-DB=Published Applications NA main -OFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext
-USER=500 -MINILEN=0 -MAXIED=200000000 -HOST=abss02h
-USER=US09827854 @CGN 1 1 2226 @runat 14062006 081838 26978 -NCPU=6 -ICPU=3
-NO MNAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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2553.658 Million cell updates/sec
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                                                                                                                                                                                            1 KVEQAVETEPEPELRQQTEW......VEKVQAAVGTSAAPVPSDNH 299
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                                                                                                    June 14, 2006, 21:46:34 ; Search time 2158.08 Seconds
              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                        - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                   18892170 segs, 6143817638 residues
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Xgapop 10.0, Xgapext
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Fgapop 6.0, Fgapext
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Maximum DB seq length: 2000000000
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Database :

Score

Result

Sequence 3787, Ap Sequence 3, Appli

Sequence 3, Appl

Sequence 126, App

Sequence 7,

Sequence 104, App

Sequence 265, Sequence 10,

Sequence 475,

Sequence 154,

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9.78e-135
1493.00
100.0%
100.0%
                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-827-854-8
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Best Local Similarity: 1
Query Match:
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       Length:
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GENERAL INFORMATION:
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
APPLICANT: Zannis, Vassilis
TITLE OF INVENTION: Compounds and methods for lowering
TITLE OF INVENTION: Cholesterol levels without inducing hypertriglyceridemia
FILE REPERENCE: 07180/004003
CURRENT APPLICATION NUMBER: US 09/679,088
PRIOR APPLICATION NUMBER: US 09/679,088
PRIOR APPLICATION NUMBER: US 09/679,088
PRIOR PLING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1156 140 160 180 200 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100 414 120 474 594 654 714 174 354 294 9 80 115 AAGGTGGAGCGAAGCGGTGGAGACAGAGCCGGAGCCGGAGCTGCGCCCAGCAGAGCGGTGG GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 235 CAGACACTGTCTGAGCAGGAGGAGGAGCTGCTCAGCTCCCAGGTCACCCAGGAACTG CAACTGACCCCGGTGGCGGAGAGAGACGCGGGCACGGCTGTCCAAGGAGCTGCCAGGCGGCG GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly CAGGCCCGGCTGGGCGCGCGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly CTGGGGCCCCTGGTGGAACAGGGCCGCGTGGGCCGCCACTGTGGGCTCCCTGGCCGGC GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 1156 299 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-827-854A-2 (1-299) x US-09-827-854-8 (1-1156)

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CAGGCCCGGCTGGGCCGCGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC
                                           GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
                                                             GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCAC
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                                                                                                                                                                                                                                                                                                    LOCATION: (61)...(1014)
OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein
OTHER INFORMATION: (APOE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 17, Application US/09802640
| Sequence 17, Application US/09802640
| Publication No. US20030036057A1
| GENERAL INFORMATION:
| APPLICANT: Braun, Andreas
| APPLICANT: Braun, Andreas
| APPLICANT: Rleyn Patrick
| TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
| FILE REPERENCE: 24736-2048
| CURRENT FILING DATE: 2001-03-09
| CURRENT FILING DATE: 2001-03-09
| WUMBER OF SEQ ID NOS: 122
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 17
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ORGANISM: Homo sapien
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE REFERENCE: 870759
CURRENT FILING DATE: 2002-01-14
FRIOR PILING DATE: 2000-01-14
FRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 129
LENGTH: 1156
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LOCATION: (61)..(1014)
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 129
LENGTH: 1156
TYPE: DNA
ORGANISM: Homo sapiens
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; OTHER INFORMATION:
US-09-751-708A-129
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Query Match:
DB:
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Publication No. US20030157113A1
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US/09/751,708A
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Sequence 1, Application US/10313641

Sequence 1, Application US/10313641

GENERAL INFORMATION:

APPLICANT: ISAlida, Brian

APPLICANT: Bailey, Kathy

APPLICANT: Schwartz, Daniel

TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)

FILE REFERENCE: P02321US2

CURRENT APPLICATION NUMBER: US 60/415,864

PRIOR FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US 60/415,864

PRIOR PILING DATE: 2001-12-07

PRIOR SPELICATION NUMBER: US 60/415,864

PRIOR SPELICATION NUMBER: US 60/415,864

PRIOR SPELICATION NUMBER: US 60/415,864

PRIOR SPELICATION NUMBER: US 60/340,498

SOFTWARE: Patentin version 3.1

TENNOR NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1
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APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Murgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION: THERAPY OF COLON CANCER
FILE REFREENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/331,978
PRIOR PELING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
                                                   LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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Publication No. US20030148410A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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                                                                                                                                                                                                              LOCATION: (61)...(1014)
OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein
OTHER INFORMATION: (APOE)
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Matches:
Conservative:
Mismatches:
Indels:
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1493.00
100.0%
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                                                                                                                                                                      ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                              ; OTHER INFORMA'
US-10-403-902A-17
                                                                                                                                                                                                                                                                                   Alignment Scores:
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Sequence 17, Application US/10403902A
Publication No. US20030224418A1
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bansal, Aruna

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                                   GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Data:
APPLICATION DATA:
TILING DATE: 14-Aug-2003
CLASSIFICATION: CUNROWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 1007, Application US/10641643
; Publication No. US20040077003A1
; GENERL INFORMATION:
APPLICANT: Cocks, Benjamin G.
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ADDRESSEE: INCYTE PHARMACI
STREET: 3174 PORTER DRIVE
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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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US-10-641-643-1007
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Publication No. US2003029062A1

GENERAL INFORMATION:

APPLICANT: IShida, Brian

APPLICANT: Bailey, Kathy

APPLICANT: Bailey, Kathy

APPLICANT: Bailey, Kathy

APPLICANT: Schwartz, Duncial

TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)

FILE REFERENCE: P0231US3

CURRENT APPLICATION UNMBER: US/10/428,551

CURRENT FILING DATE: 2003-05-02

PRIOR FILING DATE: 2002-10-03

PRIOR FILING DATE: 2002-10-03

PRIOR FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGHT: 1156
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                           MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg
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775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGAAGGAGCAGGTGGCGGAGGTGCGC
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Human US-10-428-551-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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GRUREAL INFORMATION:

GAPLICANI: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REPRENEUES: 38373-189118

CURRENT APPLICATION NUMBER: US 60/378,988

PRIOR APPLICATION NUMBER: US 60/378,988

PRIOR PILING DATE: 2002-05-08

PRIOR PILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-15

PRIOR FILING DATE: 2002-06-09

PRIOR FILING DATE: 2002-00-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2002-10-02

PRIOR FILING DATE: 2003-01-09

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN NUMBER: US 60/438,686

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN VEXESON 3.2

SEQ ID NO 125

**MADE: NA
                                                      AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
                                                                                                                                                                  LeulysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
                                                                                           GCCAAGCTGGAGGAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC 894
                                                                                                                                                                                                  775 ATGGGCAGCCGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 834
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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US-10-428-817A-125
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Best Local Similarity:
Query Match:
DS:
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US-10-428-817A-125
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                                                                                                                  835
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUTCATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-416
INFORMATION FOR SEQ ID NO: 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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SEQUENCE DESCRIPTION: SEQ ID NO: 1007
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Sequence 1. Application US/10794198A

Publication No. US2004026663A1

Sequence 1. Application US/10794198A

Publication No. US2004026663A1

SEQUENCE INFORMATION:

APPLICANT: Schwartz, Daniel

APPLICANT: Bailey, Kathy

FILE OF INVENTION: ENTHABLIUM (RPE) AND BRUCH'S MEMBRANE (BM)

FILE REFERENCE: HO-PO2351US4

CURRENT APPLICATION NUMBER: US/10/794,198A

CURRENT FILING DATE: 2004-03-05

PRIOR FILING DATE: 2002-12-06

PRIOR PELING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR APPLICATION NUMBER: US 60/340,498

PRIOR PILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: US 60/315,864

PRIOR PILING DATE: 2002-10-03

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 1

LENGTH: 1156
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AGGGCGCTGATGGACGAGCCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAA
                     GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla
                                 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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US-10-937-758A-106
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                              Sequence 10, Application US/10852335A; Sequence 10, Application US/10852335A; Bublication No. US200S0112129A1; Bublication No. US200S0112129A1; GENERAL INFORMATION:
INFORMATION: PHILLIPS
ITILE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumors of Glial Origin; TITLE OF INVENTION: Treatment of Tumors of Glial Origin; TITLE OF INVENTION: Treatment of Tumors of Glial Origin; CURRENT APPLICATION NUMBER: US 60/548,299; PRIOR PELING DATE: 2004-05-24; PRIOR FILING DATE: 2004-05-24; PRIOR FILING DATE: 2003-05-23; PRIOR FILING DATE: 2003-05-23; NUMBER OF SEQ ID NOS: 190; SEQ ID NO 10; LENGTH: 1156
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Sequence 106, Application US/10937758A

Publication No. US20050112141A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVERTION:

CURRENT PAPLICANT: PILE REFERENCE 650884

CURRENT PAPLICATION NUMBER: US/10/937,758A

CURRENT PAPLICATION NUMBER: 09/650,884

PRIOR APPLICATION NUMBER: 09/650,884

PRIOR PILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 121

SOFTWARR: Patentin version 3.1

SEQ ID NO 106
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                     GCCAAGCTGGAGGAGGAGGCCCAGCAGAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGC
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US-10-773-446-63

Sequence 63, Application US/10773446

Dublication No. US20050176662A1

GENERAL INFORMATION:

APPLICANT: INANA, GEORGE

APPLICANT: MICLAREN
MARGARET

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

CURRENT APPLICATION WUMBER: 2091-02-09

NUMBER OF SEQ ID NOS: 131

SOFTWARE: 2004-02-09

NUMBER: OF SEQ ID NOS: 131

SOFTWARE: 1156

LENGTH: 1156

TYPE: DNA

ORGANISM: Homo sapiens

US-10-773-446-63
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                ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu
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BD02884 Sequence
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AX427528 Sequence
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BC003557 Homo sapi
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AX409597 sequence
M12529 Human apoli
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Location/Qualifiers
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I69313 Sequence 10
AR211787 Sequence
                                                June 14, 2006, 19:02:13; Search time 557.375 Seconds (without alignments) 3097.698 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                    - nucleic search, using frame_plus_p2n model
                                                                                                                                                          31973710525 residues
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Database :

Result No.

Minimum DB Maximum DB

Searched:

Homo sapien

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ASTOOLIO 117 bp DNA linear SYN 08-NOV-1996
Artificial sequence DNA for expression cassette, toolbox 10.
Y09270
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I (bases 1 to 275)

In (bases 1 to 275)

Characterization of different mRNA types expressed in human brain Unpublished

2 (bases 1 to 275)

Dmitrenko, V V.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-AR-1996) Dmitrenko V. V., Institute of Molecular
Biology and Genetics, Biosynthesis of Nucleic Acids, Zabolotnogo
150, Kiev, Ukraine, 252627
                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 117)
Schluseener, H.J.
Direct Submission
Submitted (21-OCT-1996) H.J. Schluseener, Inst.f. Hirnforschung,
Calwer Str. 3, D- 77076 Tuebingen, FRG
                                                                                                                                                                                                                                                                                                                                                    /organism="synthetic construct"
/mol_type="other DNA"
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/cransl_table=11
/product="colbox 10 expression cassette"
/protein id=CapA0465.1"
/db xref="GI:1666293"
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          1 ATGAAGGTTCTGTGGGGCTGCTTGCTGGTCACATTCCTCGCAGGATGCCAGGCC
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apolipoprotein E.
Homo sapiens (human)
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                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 71)
Shimomura, T., Yamada, K., Morimoto, Y., Kitamura, N. and Miyazawa, K.
Hepatocyte growth factor activating protease and gene encoding the protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 93)
1 (bases 1 to 93)
2 Falduco, W.T., Waganuson, S.R. and Morgan, D.W.
Human matrix metalloprotease gene, proteins encoded therefrom and methods of using same
Patent: US 6399371-A 4 04-UUN-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                     ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65
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Location/Qualifiers
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Sequence 10 from patent US 5677164.
169313 1 GI:2831435
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6399371.
AR211787.1 GI:21515202
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                            US-09-827-854A-13 (1-18) x I15467 (1-71)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 2137 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
Unclassified.
Unclassified.
(Leges 1 to 405)
Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.
Expressed sequence tags and encoded human proteins
Patent: US 6783961-A 2137 31-AUG-2004;
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Sequence 2137 from Patent EP1033401.
AX886274
     /mol_type="genomic DNA"
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/db_xref="InterPro: IPR000074"
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/db_xref="UniterPro: IPR0000
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                         /mol type="minorations" mol type="minorations" mol type="minorations" mol type="minorations" mol type="minorations" mol type="brain" /clone_lib="S: Meier-Ewert's cDNA library no. 507" /dev stage="fetus" meier-Ewert's cDNA library no. 507" /dev stage="fetus" mol type="mol type
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Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 2130 02-OCT-2001;
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02-0CT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
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/organism="Homo sapiens"
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets

Patent: WO 0194629-A 1016 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Patent: WO 9712992-A 28 10-APR-1997;
ROYAL NETHERLANDS ACADEMY OF A (NL.)
Other publication AU 7142796 970428.
Location/Qualifiers
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PATENT: WO 9712992-A 30 10-APR-1997;
ROYAL NETHERLANDS ACADEMY OF A (NL)
Other publication AU 7142796 970428.
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                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Tang,Y.T., Goodrich,R.W., Asundi,V. and Drmanac,R.T. Cathepain V-like polypeptides
Datent: US 6783969-A 876 31-AUG-2004;
Nuvelo, Inc.; Sunnyvale, CA Location/Qualifiers
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/note="Incyte ID No: 346599.9.dec"
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Matches:
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AR578700
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Matches:
         Sequence 38 from Patent W00121836.
AX427528
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                       AX427528.1 GI:21537674
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                                                                                                                                               Hominidae; Homo.
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Unclassified.
                                                                                                     Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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          LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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TITLE
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AX427528
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us-09-827-854a-13.p2n.rge

Alignment Scores: Pred. No.: Score: Percent Similarit Best Local Simila DB:	Alignment Scores: Pred. No.: Score: Percent Similarity: Dest Local Similarity: Query Match:	1.99e-08 92.00 100.0% 100.0% 100.0%	Length: Matches: Conservative: Mismatches: Indels:	660 118 0 0 0 0
US-09-827	US-09-827-854A-13 (1-18) x A62342 (1-660)	x A62342 (1	-660)	
ò	1 MetLyBVall	euTrpAlaAlaL	euLeuValThrPheLeu	1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
ΩP	62 ATGAAGGTTC	rerescrecer	TGCTGGTCACATTCCTG	62 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGTGCCAGGCC 115

Search completed: June 14, 2006, 21:46:04 Job time : 560.375 secs

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OM protein

Run on:

Sequence:

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Adm44512 Novel hum
Adc69792 Partial h
Adg71903 Human CDN
Adg71915 Human G P
Adg71915 Human G P
Adg71909 Human G P
Adg71909 Human CDN
Adj87246 Human G P
Adg71905 Human G P
Acd95309 Human col
Ac02139 Human sec
Abk34238 Human col
Adv76096 Human col
Adv76095 Human col
Ach21663 Human adu
Abh67340 Thyroid c
Abh62679 Colon ade
Abh95994 Gene #249
Adj57602 Human apo
Aas03049 Human ia
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Aaf84315 Human Apo
Aaf84314 Human Apo
Aaf84316 Human Apo
Abc13008 Human apo
Aad22047 Human apo
Aad22047 Human apo
Aad22049 Human apo
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Aad22049 Human apo
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Aan50450 Sequence
Aan60409 Human apo
Aba83113 Apolipopr
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ADG71915
ADG71909
ADG71909
ADG71907
ADG71907
ADJ87244
ADJ87244
ADJ872424
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AAT69792
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ADQ86961
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AAN50450
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(ASFR-) ASSOC FR CONTRE MYOPATHIES.
(TZAR/) TZARTOS S.
(MAMA/) MAMALAKI A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nicotinic acetylcholine recep
myasthenia gravis; ss; primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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   ADE15845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE15845
    -MODEL=frame+_p2n.model - DEV=x1h
-Q2/abss/ABSSWEB spool/US09827854/runat 14062006 081823_26716/app_query.fasta_1
-Q2/abss/ABSSWEB spool/US09827854/runat_14062006 081823_26716/app_query.fasta_1
-Q2/abss/ABSSWEB spool/US09827854/runat_14062006 081823_26716/app_query.fasta_1
-UMITS=bits = START=1 - END=-1 - MATRIX-blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OTTFMT=prc - NORM=ext - HEAPSIZE=500 - MINILEN=0 - MAX.EN=200000000 - HOST=abss04
-NORM=prc - NORM=ext - HEAPSIZE=500 - MINILEN=0 - MAX.EN=200000000 - HOST=abss04
-NO MMAP - NEG SCORES=0 - WAIT - DSPBLOČK=100 - LONGLOG - DEV TIMEOUT=120
-WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=7
-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Aav08172 Primer fo
Ab157678 Human mat
                                                                         June 14, 2006, 18:51:12; Search time 61.9495 Seconds (without alignments) 3038.776 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                     - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     5244920 segs, 3486124231 residues
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Maximum Match 100%
Listing first 45 summaries
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AAV08172
ABL57678
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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92
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Database :

Result No.

Minimum DB Maximum DB

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Producing recombinant domains of the human muscle nicotinic acetylcholine receptor (AChR) for treating myasthenia gravis, which contains the major part of the extracellular domain of the AChR receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human matrix metalloprotease gene - used to develop products for the diagnosis, prevention and treatment of e.g. cancer, arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMP19; matrix metalloprotease 19; human; cancer; arthritis; inflammation; therapy; diagnosis; PCR primer; ss.
                                                                                                                                                       The present invention relates to producing of a group of recombinant domains of the human muscle nicotinic acetylcholine receptor (AChR) subunits alpha, beta, gamma, delta and epsilon, or the mutant forms of the molecules, or the alpha domain containing the P3A exon, which contains the major part of the extracellular domain of the receptor. The method is useful for producing recombinant domains of the human muscle nicotinic AChR for the immunoadsorption of anti-AChR antibodies in myasthenia gravis patients. The permanently immobilized molecules can be used alther separately or in combination for therapeutic in vitro or exvivo elimination/apheresis of the majority of the anti-AChR antibodies from the blood or sera of MG patients. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kostelidou
                                                                                                                                                                                                                                                                                                                                                         Seguence 79 BP; 13 A; 23 C; 27 G; 16 T; 0 U; 0 Other;
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Matches:
Conservative:
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            Psaridi-Linardaki L,
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                                                                                                                                Example 4; SEQ ID NO 13; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                primer of the invention.
             Mamalaki A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-531521/45.
                                         WPI; 2003-903165/82
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                                                                                                                                                                                                                                                                                                                                                                                        gnment Scores:
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DB:
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The sequence represents a PCR primer used in the invention to amplify DNA encoding the clone 907334 matrix metalloprotease protein (MMP-ABT) from a plasmid. The invention relates to a novel polynucleotide, which comprises a nucleotide sequence encoding a human matrix metalloprotease protein (designated MMP-ABT). The protein of the invention has cytostatic, anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, useful for diagnosing, inflammatory diseases (e.g. for treating these diseases.
                                   This sequence represents a PCR primer for the human matrix metalloprotease 19 (MMP19) coding sequence of the invention. The DNA, protein, and antibodies against MMP19 can be used in the diagnosis, prognosis, prevention or treatment of individuals with conditions associated with the expression of the MMP19 gene, such as cancer, arthritis or inflammation, or to identify a predisposition to these conditions. The DNA can be fixed to a substrate and used to detect the presence of MMP19 in a sample. The sequences can be used to make primers for use in reverse transcription PCR to detect MMP19, they can also be used to identify inhibitors of MMP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human matrix metalloprotease protein MMP-ABT EST upstream PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; MMP-ABT; matrix metalloprotease; cytostatic; anti-inflammatory; anti-arthritic; gene therapy; cancer; inflammatory disease; arthritis; EST; expressed sequence tag; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                          (1-93)
              Example 3; Page 49; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FALD/) FALDUTO M T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361182/39
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL57678;
                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL576
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X & Z C C C C C C C Z X X
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inflammatory, and anti-arthritic activity. The polynucleotide may have a use in gene therapy. The MMP-ABT polynucleotides and proteins are useful for detecting, diagnosing, staging, monitoring, prognosing, preventing or treating cancer or inflammatory diseases (e.g. arthritis). The MMP-ABT proteins and polynucleotides are also useful developing therapeutic agents that affect MMP function
   886666666
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Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;

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0000
      Length:
Matches:
Conservative:
Mismatches:
Indels:
       5.1e-07
92.00
100.0%
100.0%
                              Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                      Query Match:
DB:
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## (1-93)US-09-827-854A-13 (1-18) x ABL57678

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16 ATGAAGGTTCTGTGGGCTGCTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 69
MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla
                    BP.
                    ACD95309 standard; cDNA; 333
                                  23-SEP-2003 (first entry)
                           ACD95309;
                 ACD95309
                        ò
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breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus; influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium; Open reading frame detection; genome sequencing; colon cancer; Human colon cancer cell expressed cDNA #3721.

Homo sapiens. gene; ss.

24-OCT-2002

US2002155438-A1.

99US-00406117. 98US-00196716 27-SEP-1999; 20-NOV-1998;

(SIMP/) SIMPSON A J G. (BREN/) BRENTANI R R. ы О NETO (NETO/)

Brentani RR; Neto ED, Simpson AJG,

WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human suffering from cancer involves use of single oligonucleotide primer at low stringency for preparing single-stranded cDNA from mRNA of individual.

Example 9; Page 543; 959pp; English.

The invention describes a method of determining open reading frames in the genome of organism, comprising contacting mRNA from cell of organism with a single oligonucleotide primer (I) at low stringency, preparing single-stranded cDNA by reverse transcribing mRNA with (I), amplifying cDNA, sequencing the product, and repeating the contacting, preparing and amplifying steps with different primers and sequencing resulting nucleic acids. The method is useful for: determining that a known nucleotide sequence from a genome of an organism corresponds to a

conclectide sequence of an open reading frame; for preparing a contig,

nucleic acid molecule from a genome of an organism; and for sequencing

con lor part of a genome of an organism. mRNA is obtained from meammalian

or human cell which is associated with a pathological condition e.g. a

colon cancer or breast cancer cell. The method is useful for analyses of

colon cancer or breast cancer cell. The method is useful for analyses of

colon cancer or breast cancer cell. The method is useful for analyses of

large or small populations. further, it can be used to study living

systems to determine if, e.g. there have been genetic shifts which render

conjenited diseases, and the risk of affliction to a foetus, as well as

to engenited diseases, and the risk of affliction to a foetus, as well as

the study of whether the conditions are likely to be passed to offspring

through ova or sperm. The analyses for pathological conditions can be

congenited dout in all animals, plants, birds, fish, etc. Using this method,

in the area of agriculture, for example the genomes of food crops can be

cudied to determine if resistance genes are present, defects in plant

condensation of the pathogens which integrate into the genome, such as

retroviruses and other integrating viruses such as influenza virus, have

cudergone shifts or mutations, which may require different approaches to

therapy. This method is also applied to eukaryotic pathogens; such as

crypanosomes, different types of lasmodium, etc. The method essentially

continues sequencing of non-coding portions. This leaves represents a

coliminates sequencing of non-coding portions. This leaves the sequence represents a polynucleotide isolated from human colon cancer cell cDNA library 

## Sequence 333 BP; 73 A; 83 C; 120 G; 55 T; 0 U; 2 Other;

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333
118
0
0
0
                 Matches:
Conservative:
Mismatches:
         Length:
                                              Indels:
                                                                           US-09-827-854A-13 (1-18) x ACD95309 (1-333)
        2.26e-06
                          100.0%
100.0%
                                              100.0%
                  92.00
                         Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                               Query Match:
         Pred. No.:
                   Score:
                                                                                              à
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S RESULT

AAC02139 standard; cDNA; 405 BP.

(first entry) 06-OCT-2000

Human secreted protein 5' EST, SEQ ID NO: 2137.

sequence tag, secreted protein; cDNA isolation; mapping; ss. gene therapy; chromosome mapping; expressed Human; 5' EST; 

Homo sapiens.

EP1033401-A2

06-SEP-2000.

21-FEB-2000; 2000EP-00200610

99US-0122487P 26-FEB-1999;

(GEST ) GENSET

Giordano Duclert A, Dumas Milne Edwards J,

WPI; 2000-500381/45.

P-PSDB; AAG02133

New nucleic acid that is a 5' expressed sequence tag (5' EST) for

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diagnostic, forensic, gene therapy and chromosome mapping procedures.
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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Claim 1; SEQ ID NO 2137; 71pp + Sequence Listing; English.

The present sequence is one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used to obtain full length upstream regulatory sequences and to design expression and secretion rectors

Sequence 405 BP; 90 A; 105 C; 149 G; 60 T; 0 U; 1 Other;

405 000 000 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.85e-06 100.0% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match DB:

US-09-827-854A-13 (1-18) x AAC02139 (1-405)

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## ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 128 1 MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18

ABK34238 standard; cDNA; 407 BP (first entry) 08-MAY-2002 ABK34238; RESULT 

Human cDNA for novel secreted protein, SEQ ID 7.

Human; 88; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetees; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency; lymphoid cell deficiency

Homo sapiens

WO200177290-A2.

18-OCT-2001.

29-MAR-2001; 2001WO-US010295

06-APR-2000; 2000US-0194941P

(GEMY ) GENETICS INST INC

Resnick RJ; HOWER SH, Agostino MJ, Fechtel K, JR; Wong GG, Clark HF, Gulukota K, Graham

WPI; 2002-179323/23.

Six hundred and twenty five polynucleotides derived from a variety of

The invention relates to 625 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted a variety of human tissue sources and which encode novel secreted corrected that complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell cransformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length con be used as probes for the identification and isolation of full length con a nutritional supplements. The protein is useful in the treatment of various immune deficiencies and gloorders such as viral infections, bacterial infections, fungal infections, autoimmune thyroiditis and chabetes) and allection reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's classouseful for treatment of burns, inclaions and ulcers. The proteins are also useful for regulating haematopoiesis, for treating myeloid or lapponed the form of the conditions of the foll deficiencies. The present sequence is one of the 625 cDNA conditions and ulcers. The present sequence is one of the 625 cDNA conditions. human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders. Claim 1; Page 70; 339pp; English. 

Sequence 407 BP; 88 A; 103 C; 158 G; 58 T; 0 U; 0 Other;

404 00 00 00 00 Length: Matches: Conservative: Mismatches: Indels: 2.86e-06 92.00 100.0% 100.0% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

US-09-827-854A-13 (1-18) x ABK34238 (1-407)

18 73 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 20 Š 용

ADV76096 RESULT

ADV76096;

ADV76096 standard; DNA; 440 BP.

(first entry) 10-MAR-2005

NO 2937. Human colon tumor cell downregulated gene SEQ ID

ds; gene; cancer; neoplasm; cytostatic.

Homo sapiens

WO2004110345-A2.

23-DEC-2004.

28-OCT-2003; 2003WO-US034019. 

29-OCT-2002; 2002US-0422176P.

(PHAA ) PHARMACIA CORP.

Klein BK; Hippenmeyer PJ, Bu JJ, Head RD, A, Staten NR; Bourner MJ, Bu Mazzarella RA,

WPI; 2005-039958/04.

Matches:

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ACH21663
                                                                                                                  RESULT
                                                                                                                                                      The invention relates to an antibody immunospecifically binds to peacherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents a gene downregulated in human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. The present sequence represents a gene downregulated in human colon cancer
New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                                                                                                                           Human colon tumor cell downregulated gene SEQ ID NO 2936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein BK
                                                                                                                 94 A; 114 C; 168 G; 62 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 166 G; 62 T; 0 U; 0 Other,
                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hippenmeyer PJ,
                                          ID NO 2937; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 2936; 257pp; English.
                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                         gene; cancer; neoplasm; cytostatic.
                                                                                                                                                                                                           (1-440)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RD,
                                                                                                                                                                                                                                                                                 ADV76095 standard; DNA; 441 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-2003; 2003WO-US034019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2002; 2002US-0422176P.
                                                                                                                                           3.13e-06
92.00
100.0%
100.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bu JJ, Head
A, Staten NR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 441 BP; 98 A; 115
                                                                                                                                                                                                                                                                                                                      10-MAR-2005 (first entry)
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                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                 BP;
                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                            WO2004110345-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bourner MJ, Bu
Mazzarella RA,
                                                                                                                Sequence 440
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Pred. No.:
                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-2004
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                                                                                                                                                                               Query Match:
DB:
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polyneptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences or enseit in adagnostics as expressed sequence tags (EST) for information in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations in cresponsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCK, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense bnA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data contains a part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag;
                                                                                                                                                                                                                   Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 445 BP; 98 A; 113 C; 161 G; 72 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from USPTO at
  0000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/sequence.html?DocID=20030073623
                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; sequencing by hybridisation; SBH; ex
genome mapping; biodiversity; genetic disorder.
                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 8875; 44pp; English.
                                                                                                                                                                 (1-441)
                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                 US-09-827-854A-13 (1-18) x ADV76095
                                                                                                                                                                                                                                                                                                                                                                                        ACH21663 standard; cDNA; 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adult ovary cDNA #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
92.00
100.0%
100.0%
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LABAT I.
STACHE-CRAIN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense DNA or RNA
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JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-615964/58.
                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH21663;
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(LABA/) I
(STAC/) (
(DICK/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JONE/)
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Alignment Scores:

441

Length:

3.14e-06

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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon adenocarcinoma related gene sequence SEQ ID NO:1016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-827-854A-13 (1-18) x ABL67340 (1-478)
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92.00
100.0%
100.0%
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                                                                                                                                                                                           Augustus M,
                                                                                                                                                                                                                      Weaver Z;
                                                                                                                                           (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                              WPI; 2002-188264/24.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2002
                                                                                                                                                                                 Young PE, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                             MetLysvalleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
  Thyroid cancer related gene sequence SEQ ID NO:5677.
  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                       US-09-827-854A-13 (1-18) x ACH21663 (1-445)
                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0209511P.
2000US-0233617P.
2000US-0233617P.
2000US-023403P.
2000US-023403P.
2000US-023403P.
2000US-0234527P.
2000US-0234527P.
2000US-0234527P.
2000US-0234527P.
2000US-0234527P.
2000US-0234527P.
2000US-0234527P.
2000US-023563P.
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2000US-023563P.
2000US-023563P.
2000US-023563P.
2000US-023563P.
2000US-023572P.
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3.18e-06
92.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2002 (first entry)
                                                 Percent Similarity:
Best Local Similarity:
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18-88P-2000
20-88P-2000
20-88P
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26.588P-2000;
26.588P-2000;
27.588P-2000;
27.588P-2000;
27.588P-2000;
28.58P-2000;
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                                                                                                 Query Match:
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       Pred. No.:
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                                  Score:
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478 00 00 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 954 identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data of a strenges to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                          Carter KC,
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0245084P.
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The present invention describes a method (M1) for screening for an antinopplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gne (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in AbL61664 to AbL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomed, luny, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1016; 44pp; English
                                                                                                                                                                                                                                                                                                     2000US-0235840P.
2000US-0235863P.
                                                                                                                                                  2000US-0234567P
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2000US-0237598P.
            30-MAY-2001; 2001WO-US010838
                                                                                               2000US-0234009P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-188264/24.
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02-0CT-2000;
03-0CT-2000;
03-0CT-2000;
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29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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22-SEP-2000;
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27-SEP-2000;
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28-SEP-2000;
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Soppet DR,
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Horrigan S;

Ebner R, Endress G,

Carter KC,

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cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tunmour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93603-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                     396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
                                                                                                                                                                                                                                                                                                             1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                        Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                           US-09-827-854A-13 (1-18) x ABL62679 (1-478)
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                                                                                                                                              3.45e-06
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ABN95994 standard; DNA; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-426119/45.
                                                                                                                                                                                                      Best Local Similarity:
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                                                                                                                                                                                  Percent Similarity:
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                                                                                                                             Alignment Scores:
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Seguence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;

custom

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for the custom assays, and delivering to the consumer at least one custon or stock assay in response to the order. The methods use PCR and RT-PCR procedures. The present sequence represents a human apolipoprotein E (apoE) DNA sequence.
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                                                                                                                                                                                                                       Human diagnostic and therapeutic (dithp) cDNA sequence #38.
                                                                 Sequence 480 BP; 99 A; 137 C; 178 G; 66 T; 0 U; 0 Other;
                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                               (1-480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9905-0156624P
9905-015662P
9905-0167517P
9905-0167520P
9905-016752P
9905-016752P
9905-016752P
9905-0167542P
9905-0167942P
9905-0167945P
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99US-0168611P.
99US-0168613P.
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99US-0155939P.
99US-0156294P.
99US-0156565P.
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                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 - SEP - 1999;
24 - SEP - 1999;
28 - SEP - 1999;
28 - SEP - 1999;
24 - NOV - 1999;
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24-NOV-1999;
24-NOV-1999;
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                                                                                            Alignment Scores:
Pred. No.:
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01-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides methods and assays for ordering assays which detect single nucleotide polymorphisms (SNPs) or gene expression. It provides to a consumer, assays to detect presence or expression of genetic material, by providing a web-based user interface to receive an order for one or more stock assays, providing a web-based user interface to receive a request for design of one or more custom assays and an order
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koehler RT, Livak KJ, Stevens J, De La Vega FM, Rhodes M; Bellon LR, Dalley D, Ziegle J, Williams J, Madden D, Gilbert DA Scafe CR, Avi-Itzhak HI, Webster MN, Wang YN, Spier BG, You X; Hemken H, Titus A, Ku L, Curlee J, Heil J, Glanowski S, Scott Winn-Deen E, Mccullen I, Wu L, Gire C, Sprague A, Eddins S;
                                                                                                                                                               396 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 343
                                                                                                                                              1 MetlysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; gene expression; genotyping; apolipoprotein E; apoE; human; gene; ds.
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                        Human apolipoprotein E DNA sequence.
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                                                                                                                                                                                                                            BP.
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2002US-0352356P.
2002US-0369127P.
2002US-0369657P.
2002US-0370921P.
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2002US-0380657P
2002US-0383654P
2002US-0383954P
2002US-0390708P
2002US-0394115P
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GENBANK, M10065.
                                                    Percent Similarity:
Best Local Similarity:
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28-JAN-2002;
01-APR-2002;
03-APR-2002;
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06-MAY-2002;
28-MAY-2002;
29-MAY-2002;
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                Alignment Scores:
Pred. No.:
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                                                                                 Query Match:
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Banville SC;

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, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS; Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry Chen W, Liu TF, Yap PE, Stockdreher TK, Amshey S;
Bratcher SR,
                      Hillman JL,
                                      RJ,
                                                          WT.
                                          Wright
                                                            Fong
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WPI; 2001-281607/29.

Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia.

Claim 1; Page 274; 299pp; English.

The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #38 is 1 of 71 (AAS03012-AAS03082) novel sequence 838 is 1 of 71 (AAS03012-AAS03082) novel sequence secreted in the invention. The present sequence (Incyte ID No: 3456996060) encodes a secreted and extracellular molecule. The dithp polynucleotides may be used to identify the presence of similar nucleic acids. Dithp polynucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to screen for molecules which bind to them and modulate their used to screen for molecules and the used for gene therapy of disorders such as severe combined immundeficiaency syndrome (SCID), cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX difficancies, cardiovascular disorders e-g familial hypercholesterolaemia (FH), cell proliferative disorders e-g cancers, neurodegenerative disorders e-g cancers, infectious disorders and developmental disorders. The antibodies can be used to analyse protein expression levels 

Sequence 499 BP; 107 A; 134 C; 189 G; 69 T; 0 U; 0 Other;

4499 0 0 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: 3.63e-06 92.00 100.0% 100.0% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: Score:

US-09-827-854A-13 (1-18) x AAS03049 (1-499)

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ABZ11994

RESULT 15

BP ABZ11994 standard; cDNA; 583

ABZ11994;

(first entry) 20-JAN-2003 Human polynucleotide SEQ ID NO 876.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; multiple sclerosis; immunomodulator; nootropic; neuroprotective; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.

Homo sapiens

12-SEP-2002.

05-MAR-2002; 2002WO-US005095.

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 94% sequences (ABZ1119-ABZ1206) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABR68902-ABR66849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellinaging, screening and diagnostic assays and for treating cellinaging, or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                  New polynucleotides comprising sequences assembled from expressed sequence tags (ESTS), useful for treating cell-proliferative, neurodegenerative, autonimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
                                                                                             Ren F;
                                                                                           Zhao QA, R
, Ghosh M;
                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 876; 1012pp + Sequence Listing; English.
                                                                                           Zhang J, Zl
R, Wang Z,
                                                                                       Goodrich RW, Asundi V, Zhe
a Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
                                                                                             Goodrich RW,
                05-MAR-2001; 2001US-00799451
                                                                                                            Ma
                                                                                                                                                                        WPI; 2002-759812/82.
                                                                                                              Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
                                                      (HYSE-) HYSEQ INC.
                                                                                             Zhou P,
                                                                                                                                                                                             P-PSDB; ABP69777
                                                                                             Tang YT,
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Sequence 583 BP; 138 A; 154 C; 161 G; 130 T; 0 U; 0 Other;

Alignment Scores:

directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

583 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: (1-583)US-09-827-854A-13 (1-18) x ABZ11994 92.00 100.0% 100.0% Best Local Similarity: Query Match: Percent Similarity:

rch completed: June 14, 2006, 19:10:36 time : 64.9495 secs Search c Job time

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Sequence:

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A9962652 or31f02.8
AM983864 QV3-HT036
CN277382 170005325
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CN277413 170005315
BP418358 BP418358
BQ684487 AGENCOURT
DV70547 12LUMIGEN
AA769671 ob19001.8
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AI3113059 G92208.x
AI311109 G92310.x
CN277371 170004554
AV685887 AV685887
AI126876 G955.c05.x
AV664377 AV684377
CN277400 170006001
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BF877344 QV2-ET010
BF876758 QV2-ET010
B16739120 IL3-NT028
B1040603 IL3-NT028
CN277423 170004252
BE164869 QV1-HT047
BE164912 QV1-HT047
CB153811 K EST0211
BF877136 QV2-ET010
CN277389 170004248
BR965666 IL3-NT010
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AV686644 AV686644
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AV683676 AV683676
CN277384 170005316
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7000417761214 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7858
Email: rbrandenberger@geron.com
Insert Length: 125 Std Error: 0.00.
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                BF876758
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Regenerative Medicine
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-MODEL=frame+ p2n.model -DEV=x1h
-Q=/abss/ABSSWBB spool/US09827854/runat 14062006 081827 26762/app query.fasta_1
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BF877359 QV2-ET010
CN277422 170006000
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                                                                                               // Search time 476.517 Seconds
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3168.451 Million cell updates/sec
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                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                      nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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9b_est4:::;

9b_est6:::;

9b_est7:::;

9b_est8:::;

9b_est8:::;

9b_est8:::;

9b_est8:::;

9b_gss1::;

9b_gss1::;

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Database :

Result No.

Minimum DB E Maximum DB E

Searched:

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Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN277422 216 bp mRNA linear EST 16-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 216)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="GRN_PREHEP"
hote="Oligo dT primed, full-length enriched cDNA library
from DMGO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
                                                                                                                                                                                                                                                                                                                                            Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
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118
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Insert Length: 216 Std Brror: 0.00.
Location/Qualifiers
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/mol_type="mRNA"
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CN277422
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                            1. .125
//organisma="Homo sapiens"
//organisma="Homo sapiens"
//organisma="Homo"
//tope="mRNA"
//tissue type="embryonic stem cells, embryoid bodies
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//clone libe"GRN EB"
//note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p.22), H7 (p.29), and H9 (p.26) maintained in feeder-free
conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

Hominidae; Homo.

1 (Dases 1 to 177)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., Bordin, S., Costa, F.F., Ragal, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OV2-ET0106-161100-475-f12 ET0106 Homo sapiens cDNA, mRNA sequence.
BF877359
BF877359.1 GI:12267489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=GV2&t2=QV2-ET0106-I10100-475-f12&t3=2000-11-16&t4=1)
Seg primer: puc 18 forward
High quality sequence stop: 177.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .177
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/clone lib="BT0106"
/note="Organ: lung_tumor; Vector: puc18; Site_1: Smal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
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         Location/Qualifiers
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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AUTHORS
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           FEATURES
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL PUBMED

COMMENT

TITLE

LOCUS DEFINITION

BF877229/c

RESULT 4

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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Ono. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 221)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., Bosliva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Harte, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-161100-475-bo6&t2=2000-11-16&t4=1)
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High quality sequence.stop: 221.
  BF877344 221 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-161100-475-b06 ET0106 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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                                                                               BF877344.1 GI:12267474
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Best Local Similarity:
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  LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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AUTHORS
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PUBMED
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .221
/ organism="Homo sapiens"
/ mol type="mRNA"
/ db xref="taxon:9606"
/ dev_stage="Adult"
/ clone llb="EF0106"
/ note="Organ: lung tumor; Vector: puc18; Site_l: Smal;
/ note="Organ: lung tumor; Vector: puc18; Site_l: Smal;
/ note="Organ: lung ini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                         Hominidae, Homo.

1 (Dases 1 to 221)

Diase Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.R.,

Magai, M.A., da Sllva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                         BF877229 221 bp mRNA linear EST 17-JAN-2001
QV2-ET0106-151100-478-b01 ET0106 Homo sapiens cDNA, mRNA sequence.
BF877229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-16ttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-16ttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-16ttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-16ttp://www.ludwig.org.loog.11-15&t4=1)
High quality sequence stop: 221.
                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Best Local Similarity:
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FEATURES

Query Match:

BF877344/c

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Pred. No.:

ORIGIN

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Hominidae, Homo.

1 (bases 1 to 227)

Dias Neto, B., Garcia, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922

Fax: +55-11-2707001

Email: saimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-161100-474-gll&t3=2000-11-16&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 223.
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IL3-NT0280-240101-418-F05 NT0280 Homo sapiens cDNA, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rus Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                  Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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Homo sapiens
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Best Local Similarity:
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AUTHORS
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KEYWORDS
SOURCE
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BI039120
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dw_xref="taxon:9606"
/dw_xref="taxon:9606"
/dw_xref="taxon:9606"
/dw_xref="taxon:9606"
/dov="taxon:9606"
/dov="lorgan: lung tumor; Vector: puc18; Site 1: Smal;
/note="forgan: lung tumor; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
Site 2: Smal; A mini-library was made by cloning products
Site 2: Smal; A mini-library was made by cloning products
Site 3: Smal; A mini-library was made by cloning products
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QV2-ET0106-161100-474-gl1 ET0106 Homo sapiens CDNA, mRNA sequence.
BF877285
                                                                                                                             Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsteain,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 223)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
141100-474-q911&t3=2000-11-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 223.
High quality sequence stop: 223.
                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Concact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                           Hominidae; Homo.
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/note=_Organ: nervous tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Parent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                  Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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17000425248791 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN277423
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Geron Corporation
230 Constitution Drive, Menlo Park, CA
Tel. 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 243 Std Error: 0.00.
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1 (bases 1 to 243)
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/clone_lib="NT0280"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
/note="Organ: nervous tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cubMA amplification were performed under
low stringency conditions."
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1 (bases I to 230)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., G.Yare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                             Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence derived from the FAPESP/LICR Human Cancer Genome
This sequence are derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-NT0280-
240101-418-FOS&t2=2001-01-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 227.
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mRNA sequence.
                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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BI040603
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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EST 16-MAY-2004

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/organism="Homo sapiens"
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Fax: +55-11-2707001

Bmail: asimpsom@ludig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVl-HT0471-280

300-121-f07&t3=200.03-2&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 256.

1. .256
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BE164912
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(Loases I to 256)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QVl-HT0471-270 300-121-f07&t3=200-03-27&t4=1)
Seq primer: puc 18 forward
High quality sequence stort: 12
High quality sequence stort: 12
High quality sequence story: 256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 bp mRNA linear EST 21-JUN-2000 QVI-HT0471-270300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence. BE164869 GI:8627590 BE164869.1 GI:8627590
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1 (Bases I to 256)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., GO'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
      /db_xref="taxon:9606"
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and H9 (p26) maintained in feeder-free conditions"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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RESULT 13

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ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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/organism="Homo sapiens"

mol_type="mRNA"

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/clone_lib="ET0106"

/note="forgan: lung_tumor; Vector: puc18; Site 1: Smal;

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."
                                                                                                                                                                                            Hominidae, Homo.

1 (Dases 1 to 273)

Dias Neto,E., Garcia,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A. da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-151100-477-f05&t2=2000-11-15&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 273.

Location/Qualifiers
            BF877186 277-£05 ET0106 Homo sapiens cDNA, mRNA sequence.
BF877186
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                   269 bp mRNA linear EST 29-JAN-2003
K-EST0211405 L17N670205 Homo sapiens cDNA clone L17N670205-6-G09
5', mRNA sequence.
CB153811
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21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
FS Beeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="Top10F'"
/clone lib="Lil7N670205"
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Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mismatches:
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                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: yongsung@mail.kribb.re.kr
Plate: 6 row: 6 column: 09
High quality sequence stop: 269.
Location/Qualifiers
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Homo sapiens (human)
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                                Percent Similarity:
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Query Match:

RESULT 14

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us-09-827-854a-13.p2n.rst

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Site_2: Smal; A Mini-library was made by cloning products
Site_2: Smal; A Mini-library was made by cloning products
Garived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                          Hominidae, Homo.

1 (bases 1 to 274)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Email: assimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV2&t2=QV2-ET0106-151004-478-c04&t23=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 274.
  Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rus Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

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Sequence 10, Application US/08148910

Patent No. 5466593

GENERAL INFORMATION:
APPLICANT: Takeshi SHIMOMURA et al.
TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                 Sequence
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US-09-949-016-118246
US-09-949-016-15019
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 KD Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2665
18031
54444
109690
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3805
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                                                CITY: Washi
STATE: D.C.
COUNTRY: U.
ZIP: 20005
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US-08-148-910-10
   June 14, 2006, 19:03:31; Search time 18.795 Seconds (without alignments) 2687.952 Million cell updates/sec
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Sequence 4, App
Sequence 2137,
Sequence 2491,
Sequence 28, Ap
Sequence 28, Ap
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|EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
|EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
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                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                               - nucleic search, using frame_plus_p2n model
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US-08-448-937A-10
US-09-391-104-4
US-09-513-9996-2137
US-09-880-107-2491
US-09-799-451-876
US-08-726-306A-28
US-10-211-689-29
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Result Š. 9976, Ap 12505, A 14207, A

197665,

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1169, Ap 2304, Ap 1, Appli

1386, Ap 3, Appli

31, 1007, Ar Appli

51, Appl 51, Appl 7011, Ap 7153, Ap 2604, Ap 12815, A

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human
, ORGANISM:
US-08-448-937A-10
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US-09-391-104-4
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                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: mucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid (synthetic DNA)
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: DO KD Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,937A
FILING DATE: May 24, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: No. 56/7164ember 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
RESERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Gaps:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEX:
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Best Local Similarity:
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Pred. No.:
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DB:
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MS-09-513-999C-2137

Sequence 2137, Application US/09513999C

Sequence 2137, Application US/09513999C

Sequence 2137, Application US/09513999C

Sequence 2137, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Dollert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PILLE REPERENCE: 59.102.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                                                                                                                             12 ATGAAGGTTCTGTGGGCTGCGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 65
                                                                                                                                                                                         1 MetLysvalleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla
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                                                                                                                                                                                                                                                                                               US-UY-191-104-4

; Sequence 4, Application US/09391104
; Patent NO. 6399371.
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Magnaueon, Soctt R.
; APPLICANT: Magnaueon, Soctt R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: RYOTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REPERBNCE: 6073.US.Pl
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 93
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Matches:
Conservative:
Mismatches:
Indels:
                                        Conservative:
Mismatches:
Indels:
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  Length:
Matches:
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1.54e-08
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                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Sequence 28, Application US/08726306A

Patent No. 5598684

GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Grosveld, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
                                                                                                                                                                                                                                                                      APPLICANT: Xee, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Mang, Yunqing
APPLICANT: Yanazaki, Victoria
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Nombong
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, No. 678369e1
APPLICANT: Drimanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PLE-LE-Genes Version 2.0
LENGTH: 583
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                 ; Sequence 876, Application US/09799451; Patent No. 6783969; GENERAL INFORMATION:
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APPLICANT: Zhou, Ping
APPLICANT: Goodzich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (100)..(423)
US-09-799-451-876
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Best Local Similarity:
Query Match:
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US-09-799-451-876
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US-09-880-107-2491/C

US-09-880-107-2491/C

Sequence 2491, Application US/09880107

Sequence 2491, Application US/09880107

GENERAL INFORMATION:

APPLICANT: Wockley, Joseph G.

APPLICANT: Scherf, Uwe

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-10-06-14

PRIOR FILING DATE: 2000-10-06-14

SEQ ID NO 2491

SEQ ID NO 2491

LENGTH: 478
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COTHER INFORMATION: n = a or c or g or t
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: UNSURE
LOCATION: 20
OTHER INFORMATION: Xaa=Glu or Gln
US-09-513-999C-2137
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92.00
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100.0%
                                                                         TYPE: DIA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: 119..403
FEATURE: NAME/KEY: misc_feature LOCATION: 176
OTHER INFORMATION: s=g or c
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2137
LENGTH: 405
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Pred. No.:
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CITY: Boston
STATE: MA
COUNTRY: US
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FILE REFERENCE: 21402-416B

CURRENT APPLICATION NUMBER: US/10/211,689

CURRENT FILING DATE: 2003-01-21

PRIOR PILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-08-09

PRIOR PILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-02-16

PRIOR PILING DATE: 2002-04-16

PRIOR PILING DATE: 2002-04-16

PRIOR PILING DATE: 2002-03-13

PRIOR PILING DATE: 2002-05-15

PRIOR PILING DATE: 2002-05-15

PRIOR PAPLICATION NUMBER: 60/331,979

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2002-05-16

PRIOR PILING DATE: 2002-05-16

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, David W.
Boldog, Ferenc L.
Burgess, Catherine E.
Casman, Stacie J.
Edinger, Shlomit R.
Gangolli, Esha A.
Gorman, Linda
Guo, Xiaojia (Sasha)
Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
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APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
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; LOCATION: (18)..(599)
US-10-211-689-29
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US-10-211-689-41
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LENGTH: 684
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APPLICANT:
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DB:
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
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                                                                          MEDIUM TYPE: Discrete, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1

GURRENT PPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-oct-1996
FILING DATE: 02-oct-1996
FILING DATE: 02-oct-1995
FILING DATE: 02-oct-1996
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M. REGISTRATION NUMBER: 96,048-A (3255/00784)
TELEPHONE: (617) 345-9100
TELEPHONE: (617) 345-9101
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                                                                    Diskette, 3.50 inch, 1.44 Mb storage
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6974684
GENERAL INFORMATION:
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Burgess, Catherine E.
Casman, Stacie J.
Edinger, Shlomit R.
Gangolli, Esha A.
Gorman, Linda
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Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glenda
Spytek, Kimberly A.
Vernet, Corine A. M.
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           ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity:
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Pred. No.:
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APPLICANT:
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APPLICANT: Rieger, Daniel K.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Richard A.
APPLICANT: Shinkers, Corine A. M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Mai
TITLE REFERENCE: 21402-416B
CURRENT APPLICANTION NUMBER: 00/31/21,689
CURRENT APPLICATION NUMBER: 00/31/21
FRIOR FILING DATE: 2001-08-10
FRIOR FILING DATE: 2001-08-10
FRIOR FILING DATE: 2001-08-09
FRIOR FILING DATE: 2001-08-09
FRIOR PLING DATE: 2001-08-09
FRIOR APPLICATION NUMBER: 60/310,795
FRIOR APPLICATION NUMBER: 60/310,795
FRIOR APPLICATION NUMBER: 60/310,795
FRIOR FILING DATE: 2002-08-16
FRIOR PLING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR PLING DATE: 2002-08-16
FRIOR FILING DATE: 2002-08-16
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-13
FRIOR FILING DATE: 2001-08-14
FRIOR FILING DATE: 2001-08-15
FRIOR APPLICATION NUMBER: 60/381,030
FRIOR FILING DATE: 2001-08-15
FRIOR APPLICATION NUMBER: 60/381,030
FRIOR FILING DATE: 2001-08-15
FRIOR APPLICATION NUMBER: 60/381,030
FRIOR PRIOR APPLICATION NUMBER: 60/381,030
FRIOR PRIOR PRIOR DATE: 2001-08-15
FRIOR APPLICATION NUMBER: 60/381,030
FRIOR PRIOR PRIOR DATE: 2001-08-15
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edinger, Shlomit R. Gangolli, Esha A. Gorman, Linda Guo, Xiaojia (Sasha) Khramsrov, Nikolai V. Lepley, Denise M.
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APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine B.
APPLICANT: Casman, Stacie J.
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ORGANISM: Homo sapiens
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Query Match:
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; NAME/KEY: CDS
; LOCATION: (2).
US-10-211-689-35
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                              APPLICANT: Vornet, Corine A. M.
APPLICANT: Vornet, Corine A. M.
APPLICANT: Stoney, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
FILE REPERBNCE: 21400-416B
FILE REPERBNCE: 21400-416B
FILE REPERBNCE: 2100-08-1021
PRIOR APPLICATION NUMBER: 60/311/51
PRIOR APPLICATION NUMBER: 60/310/395
PRIOR APPLICATION NUMBER: 60/310, 795
PRIOR APPLICATION NUMBER: 60/311, 292
PRIOR APPLICATION NUMBER: 60/311, 292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311, 292
PRIOR FILING DATE: 2002-02-03
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/311, 979
PRIOR APPLICATION NUMBER: 60/311, 979
PRIOR APPLICATION NUMBER: 60/311, 979
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-31
PRIOR FILING DATE: 2001-09-31
PRIOR FILING DATE: 2001-09-13
PRIOR PRIOR FILING DATE: 2001-09-13
PRIOR PRIOR
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Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Holdey, Denise M.
APPLICANT: Hachowy, Nikolai V.
APPLICANT: Hachowy, Nikolai V.
APPLICANT: Pepley, Denise M.
APPLICANT: Pepley, Denise M.
APPLICANT: Pepley, John R.
APPLICANT: Pepman, John R.
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
                 Vernet, Corine A. M.
Voss, Edward Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (2)..(709)
US-10-211-689-41
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US-10-211-689-35
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LENGTH: 709
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APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Rieger, Daniel K.
APPLICANT: Shimkers Richard A.
APPLICANT: Shimkers Richard A.
APPLICANT: Shimkers Richard A.
APPLICANT: Shimkers K. Richard A.
APPLICANT: Shimkers Spytek, K. Rimberly A.
APPLICANT: Voss. Edward Z.
APPLICANT: Voss. Edward Z.
APPLICANT: Long, Meir Corine A. M.
APPLICANT: Dang, Meir Corine A. M.
APPLICANT: Now THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC.
ITILE REFERENCE: 2104-06-10
FILING DATE: 2001-06-10
FRIOR APPLICATION NUMBER: 00/310, 802
FRIOR PILING DATE: 2001-06-08
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2002-04-16
FRIOR FILING DATE: 2002-04-16
FRIOR FILING DATE: 2002-04-16
FRIOR FILING DATE: 2002-04-16
FRIOR FILING DATE: 2002-06-15
FRIOR FILING DATE: 2003-09-21
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Sequence 1007, Application US/09023655;
Patent No. 6607879;
GENERAL INFORMATION:
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                                          Guo, Xiaojia (Sasha)
Khramstov, Nikolai V.
Lepley, Denise M.
MacDougall, John R.
Pena, Carol A.
Peyman, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.88e-07
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ORGANISM: Homo sapiens
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LENGTH: 802
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APPLICANT:
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APPLICANT:
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APPLICANT: MacDougall, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, John A.
APPLICANT: Pertural John Mer.
APPLICANT: Shimkee; Richard A.
APPLICANT: Costine A. M.
APPLICANT: Vose, Edward Z.
APPLICA
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Sequence 31, Application US/10211689
Patent No. 6974684
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess Catherine E.
APPLICANT: Burgess, Catherine E.
APPLICANT: Gangui, Stacle J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.82e-07
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (18)..(704)
US-10-211-689-33
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Best Local Similarity:
Query Match:
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LENGTH: 788
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Query Match:
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TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE NUMBER OF SEQUENCES: 1508

CORRESPONDENCES: 1508

CORRESPONDENCES: 1314 PORTER PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
COUNTRY: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC-DOS/MS-DOS
SOFTWARE: Mord Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRILNG APPLICATION DATA:
PRILNG APPLIC
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| Sequence 1, Application US/07709949 |
| Sequence 1, Application US/07709949 |
| Patent No. 5472858 |
| GENERAL INFORMATION: |
| APPLICANT: Attie, Alan D |
| APPLICANT: Gretch, Daniel G |
| APPLICANT: Sturley, Stephen L |
| APPLICANT: Beckage, Nancy E |
| TITLE OF INVENTION: Production of Recombinant Proteins in TITLE OF INVENTION: Insect Larvae |
| WUMBER OF SEQUENCES: 2 |
| CORRESPONDENCE ADDRESS: 2 |
| ADDRESSEE: Quarles & Brady |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zealer, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEFONNE: (650) 845-4166
INFORMATION FOR EGD 10. 1007:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Quarles & Brady STREET: P.O. Box 2113
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Best Local Similarity:
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STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-023-655-1007
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Pred. No.:
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DB:
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62 ATGAAGGTTCTGTGGGGTTGCTGGTCACATTCCTGGCAGGATGCCAGGCC 115
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Patent No. 6974667

GENERAL INPORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14
COMPUTER: PSJOULISIS
COMPUTER: PLOPDY disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPDY disk
COMPUTER: PERDALELE
COMPUTER: PERDALELE
COMPUTER: PERDALELE
COMPUTER: PERDALELE
SOFTWARE: PATENTION NOTA:
APPLICATION NUMBER: US/07/709,949
FLING DATE: 19910604
CLASSIFICATION: 1935
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 9629691801
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157
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Matches:
Conservative:
Mismatches:
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Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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92.00
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc signal
LOCATION: 62..119
PUBLICATION INFORMATION:
AUTHORS: McLean, J W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 62..1015
FEATURE:
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VOLUME: 2
PAGES: 64
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| PRIOR APPLICATION NUMBER: US 60/237,054
| PRIOR FILING DATE: 2000-10-02
| NUMBER OF SEQ ID NOS: 3950
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2244
| LENGTH: 1157
| TYPE: DATE: TYPE: DATE: D
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Search completed: June 14, 2006, 19:16:12 Job time : 20.795 secs

Appli Appli Appli Appl

OM protein

Run on:

Sequence:

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Sequence 2937, Ap
Sequence 2936, Ap
Sequence 8875, Ap
Sequence 374, App
Sequence 1016, Ap
Sequence 1016, Ap
Sequence 1016, Ap
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Sequence 125, App
Sequence 1, Appli
Sequence 106, App
Sequence 63, App
Sequence 5, Appli
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Sequence 1, Appli
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Sequence 1007, Ap
Sequence 155, App
Sequence 1, Appli
Sequence 3278, Ap
Sequence 8950, Ap
Sequence 7, Appli
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Sequence 2244, Ap
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Sequence 409, App
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Sequence 129, App
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Sequence 129,
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| Sequence 4, Application US/09391104
| Publication No. US20020031817A1
| GENERAL INFORMATION:
| APPLICANT: Palduco, Michael T.
| APPLICANT: Mangan. Douglas M.
| TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS TITLE OF INVENTION: OF USING SAME
| FILE REFERENCE: 6073.US.Pl
| CURRENT PRILING DATE: 1999-09-07
| PRIOR FILING DATE: 1997-03-11
                                                                                                                                  0 US-10-843-641A-5677

US-10-11-689-29

US-10-211-689-31

US-10-211-689-31

US-10-211-689-33

US-10-211-689-33

US-10-211-689-33

US-10-211-689-33

US-10-257-021-63

US-09-827-854-10

US-09-827-854-10

US-09-827-854-11

US-10-428-551-1

US-10-428-551-1

US-10-428-551-1

US-10-428-8174-125
                          US 09-823-245A-7
US-10-696-639-2937
US-10-696-639-2936
US-09-918-995-8875
US-09-964-82AA-374
US-09-880-107-2491
US-09-873-367C-1016
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US-10-937-758A-106
US-10-773-446-63
US-11-186-284-5
US-11-055-309A-1
                                                                                                                         US-10-843-641A-1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 93
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 TYPE: DNA
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-MODEL=frame+_p2n.model -DEV=xlh
-Q={absgRABSWHES spool/180982784/runat_14062006_081838_26978/app_query.fasta_1
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-DB=Published_Applications NA Main -QFMT=fastap_SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LCOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=Dlosume2 -TRANS=bumma140.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIND=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=ppto -NORM=ext
-HEAPSIXE=500 -MINILEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US09827854 @CGN 1 1 2326 @runat 14062006 081838 26978 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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                                                                                        June 14, 2006, 21:46:34; Search time 129.918 Seconds (without alignments) 2553.658 Million cell updates/sec
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             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                  - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                           18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-391-104-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              1 MKVLWAALLVTFLAGCQA 18
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                 US-09-827-854A-13
92
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Match Length DB
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Database :

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Minimum DB Maximum DB

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100.0%
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   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                     Query Match:
DB:
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Sequence 8950, Application US/10995561
Sequence 8950, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: BETCO 1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8950
                                                                                                                                                                                                                                                                                                          Sequence 3278, Application US/10741601
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| TITLE OF INVENTION: GENERAL ENGINE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CL001500
| CURRENT FILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 26415
| SEQ ID NO 3278
| LENGTH: 201
| TITLE OF LINGE DATE: 201
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Matches:
Conservative:
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Matches:
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                                                                                                                                                   Gaps:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-10-741-601-3278
                                                                               Percent Similarity:
Best Local Similarity: 1
Query Match:
DB:
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Best Local Similarity:
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US-10-741-601-3278
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Pred. No.:
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Pred. No.:
     US-09-391-104-4
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DB:
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RESULT 5
US-10-696-639-2937
Sequence 2937, Application US/10696639
Sequence 2937, Application US/10696639
GENERAL INFORMATION:
THILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: 108/0/1
CURRENT APPLICATION NUMBER: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2002-10-29
NUMBER: OF SEQ ID NOS: 3114
SOUTHWARE: PATENTION 3.11
SEQ ID NO 2937
LENGTH: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Craft, Interly
APPLICANT: Mostino, Michael J.
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Gulukota, Kamalaka J.
APPLICANT: Gulukota, Kamalaka J.
APPLICANT: Graham, James R.
APPLICANT: Grah
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Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
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Score: 92.00
Percent Similarity: 100.0$
Query Match: 100.0$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wong, Gordon G. APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-823-245A-7
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PEATURE:
NAME/KEY: misc_feature
CCATION: (1)...(445)
OTHER INFORMATION: n = A,T,C or (US-09-918-995-8875)
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      ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-964-824A-374/c
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US-09-880-107-2491/c
                                                                                                                  Alignment Scores:
Pred. No.:
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Pred. No.:
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Sequence 2936, Application US/10696639

Publication No. US20050037439A1

GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.
ITILE OF INVENTION: DELYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
FILE REPERENCE: 01040/1

CURRENT APPLICATION NUMBER: US/10/696,639

CURRENT FILING DATE: 2003-10-29

PRIOR PELICATION NUMBER: 60/422,176

PRIOR FILING DATE: 2002-10-29

NUMBER OF SEQ ID NOS: 3114

SEQ ID NO 2936

LENGTH: 441
                                                                                                                                                                                                                                            1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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Sequence 8875, Application US/09918995

PUBLICATION OF USZO030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OFFILE OF INVENTION: ROW VARIOUS CDNA LIBRARIES

FILE REPERENCE: 20411-756

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/918,995

CURRENT PILING DATE: 1999-01-20

PRIOR PILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PRESENCE OF Windows Version 3.0

SEQ ID NO 8875
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Conservative: (
Mismatches: (
Indels: (
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Matches:
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; NAME/KEY: misc_feature
LCATION: (339)...(412)
; CTHER INFORMATION: n=unknown
US-10-696-639-2937
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CORGANISM: homo sapiens
US-10-696-639-2936
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Sequence 374, Application US/09964824A

Sequence 374, Application US/09964824A

Patent No. US20020102531A1

GENERAL INFORMATION:

APPLICANT: HOTRIGA.

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: UNMBER: US/09/964,824A

CURRENT PELING DATE: 2001-09-27

PRIOR PELING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR PELING DATE: 2000-09-28

PRIOR PELING DATE: 2000-09-28

PRIOR PELING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,026

PRIOR PELING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,026

PRIOR PRIOR APPLICATION NUMBER: US/60/236,026

PRIOR PRIOR APPLICATION NUMBER: US/60/236,026

PRIOR PRIOR APPLICATION UMBER: US/60/236,026

PRIOR PRIOR APPLICATION UMBER: US/60/236,026

PRIOR APPLICATION UMBER: US/60/236,026

PRIOR APPLICATION UMBER: US/60/236,026
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

// LOCATION: (1)...(478)

// OTHER INFORMATION: n=a,t,g or c

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Matches: Conservative: Mismatches: Indels:

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US-09-827-854A-13 (1-18) x US-09-873-367C-1016 (1-478)
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US-09-873-367C-1016/C

US-09-873-367C-1016/Application US/09873367C

Sequence 1016, Application US/09873367C

Publication No. US20030165839A1

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel

APPLICANT: BENdress, Gregory

APPLICANT: Endress, Gregory

APPLICANT: Carrer, Kenner

APPLICANT: Carrer, Kenner

APPLICANT: Carrer, Kenner

APPLICANT: Signature Gene Determination and Therapeutic Screening Using

TITLE OF INVENTION: Signature Gene Sets

TITLE OF INVENTION: Signature Gene Sets

TITLE OF INVENTION: Signature Gene Sets

FILE REPERENCE: 689290-64

CURRENT FILING DATE: 2003-04-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-01-01

PRIOR PLILING DATE: 2000-11-01

PRIOR PLILING DATE: 2000-11-01
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REPERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR PAPLICATION NUMBER: US 60/211,379 PRIOR APPLICATION NUMBER: US 60/217,054 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR PILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Genbank Accession No. US20020142981A1 N33009
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Matches:
Conservative:
Mismatches:
Indels:
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LOCATION: (1)..(478)

1 OTHER INDEMATION: n = a or c or g or

US-09-880-107-2491
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US-09-873-367C-1016
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NAME/KEY: misc feature
LOCATION: (1)...(478)
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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Best Local Similarity:
Query Match:
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Sequence 1016, Application US/10843641A

Fublication No. US20050064454A1

Sequence 1016, Application US/10843641A

SEQUENCE 1016, Application No. US2005006454A1

ITLE OF INVENTION: Signature Gene Sets

ITLE OF INVENTION: Signature Gene Sets

FILE REPERENCE: 689290-189

CURRENT PELING DATE: 2001-06-05

FRIOR PILING DATE: 2001-06-05

FRIOR PELING DATE: 2001-09-18

FRIOR PELING DATE: 2001-09-25

FRIOR PELING DATE: 2001-09-27

FRIOR PELING DATE: 2001-10-03

FRIOR PELING DATE: 20
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Conservative:
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US-10-843-641A-5677/c
; Sequence 5677, Application US/10843641A
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; OTHER INFORMATION: n=a,t,g or
US-10-843-641A-1016
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ORGANISM: Homo sapiens
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APPLICANT: VOSE, Edward Z.
APPLICANT: ACINC, VOSE, Edward Z.
APPLICANT: ALGORG, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE OF INVENTION: THEAPLE STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ATGAAGGTTCTGTGGCGTGCGTTGCTGCTACCTGGCAGGATGCCAGGCC 109
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Beldog, Ferenc L.
APPLICANT: Beldog, Ferenc L.
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: PL FL_genes Version 2.0
SEQ ID NO 876
LENGTH: 583
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Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
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Vernet, Corine A. M.
Voss, Edward Z.
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; LOCATION: (100)..(423)
US-10-302-172-876
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
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Publication No. US20040053250A1
Publication No. US20040053250A1
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Dimanac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1e1 Arginine-rich Protein-like Nucleic Acids ar
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803_LCNCP
CURRENT PAPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-03-11-21
PRIOR APPLICATION NUMBER: US/10/225,251
PRIOR PAPLICATION NUMBER: C002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
                                                  APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE BEFERENCE: 69230-189
CURRENT FILING DATE: 2004-05-12
FRIOR APPLICATION NUMBER: US/09/983,641A
CURRENT FILING DATE: 2001-06-05
FRIOR PELING DATE: 2001-06-05
FRIOR FILING DATE: 2001-09-18
FRIOR FILING DATE: 2001-09-18
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR PELING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: US/09/962,832
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-26
FRIOR FILING DATE: 2001-09-28
FRIOR FILING DATE: 2001-09-38
FRIOR FILING DATE: 2001-09-38
FRIOR FILING DATE: 2001-01-0-38
FRIOR FILING DATE: 2001-10-03
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// LOCATION: (1)...(478)
// CTHER INFORMATION: n=a,t,g or c
US-10-843-641A-5677
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LENGTH: 478
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1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
PRIOR APPLICATION NUMBER: 60/380,970
PRIOR FILING DATE: 2002-05-15
PRIOR PLING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2002-06-13
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR FILING DATE: 2001-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOFTWARE: CURASEQLIST VERSION 0.1
SEQ ID NO 41
LENGTH: 709
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Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (2).
US-10-211-689-41
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Shong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REPRENCES: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT APPLICATION DATE: 2003-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetLysValleuTrpAlaAlabeuLeuValThrPheLeuAlaGJyCysGlnAla 18
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PRIOR APPLICATION NUMBER: 60/381,030
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/323,944
PRIOR FILING DATE: 2001-09-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 132
SOPTWARE: Curasequist version 0.1
SEQ ID NO 29
LENGTH: 684
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Mismatches:
Indels:
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Matches:
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PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-211-689-41
; Sequence 41, Application US/10211689
; Publication No. US20030232347A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Rerenc L.
APPLICANT: Gasman, Stacie J.
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Grow, Xiaojia (Sasha)
APPLICANT: MacBougali, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Pena, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patturajan, Meera
Rieger, Daniel K.
Shimkets, Richard A.
Smithson, Glennda
Spytek, Kimberly A.
Vernet, Corine A. M.
Voss, Edward Z.
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                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 1
Best Local Similarity: 1
Query Match:
                                                                                                                                                                                                                                                                      NAME/KEY: CDS
; LOCATION: (18)..(599)
US-10-211-689-29
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26166, 7 490, App 18852, A 27158, A 21820, A 442, App 1, Appli

25053, A 13084, A 27239, A 15333, A 24003, A 2653, Ap 21253, Ap

Sequence

7083, Ap 14774, A 8, Appli 297, App 166913,

79433, A 12686, A 18815, A 13080, A 22075, A

80129, A 2087, Ap 8455, Ap 18066, A 36046, A 20458, A

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Sequence Sequence Sequence

OM protein

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Sequence 1, Application US/10524021

Sequence 1, Application US/10524021

Bublication No. US20060099590A1

GENERAL INFORMATION:

APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
APPLICANT: YAMADA, Yoshiji

APPLICANT: YAMADA, Yoshiji

TITLE OF INVENTION: Intervention
TITLE OF INVENTION: Intervention

FILE REFERENCE: C0200501

CURRENT APPLICATION NUMBER: US/10/524,021

CURRENT FILING DATE: 2005-02-09

PRIOR APPLICATION NUMBER: UP P2002-233041

PRIOR APPLICATION NUMBER: JP P2002-233041

SOFTWARE: Patentin version 3.1

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US-10-449-902-21253
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US-10-449-902-21253
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US-10-449-902-1429
US-11-233-697-1429
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US-11-2449-902-24150
US-11-2449-902-24150
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       Score:
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-MODEL-frame+ pan. model - DEV-x1h
-Qc_Abss/ABSWRBs spool/US09827854/runat 14062006 081840_27029/app_query.fasta_1
-Qc_Abss/ABSSWRBs spool/US09827854/runat_14062006 081840_27029/app_query.fasta_1
-DB-Published Applications NA New "OFMT=fastap - SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100
-THR MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFMT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0
-MAXIEN=200000000 - HOST=abss04
-USR=US09827854 @CGN 1 1 39 @runat 14062006 081840_27029 - NCPU=6 - ICPU=3
-USR=US09827854 @CGN=0 - NAIT - DSPBLÖCK=100 - LONGLOG - DEV TIMEOUT=120
-WARN TIMEOUT=30 - THRRADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPEXT=7
-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 18081, A
Sequence 22323, A
Sequence 64, Appl
Sequence 37, Appl
Sequence 28383, A
Sequence 10702, A
Sequence 10702, A
                                                                                                                                                                                           (without alignments)
2035.043 Million cell updates/sec
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1. / ENC_Celerra SIDS3/ptodata/2/pubpna/US09 NEW PUB.seq:*
2. / ENC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW PUB.seq:*
3. / ENC_Celerra_SIDS3/ptodata/2/pubpna/US07 NEW PUB.seq:*
4. / ENC_Celerra_SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:*
5. / ENC_Celerra_SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:*
6. / ENC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7. / ENC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8. / ENC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                     ; Search time 3.12303 Seconds
                           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                       - nucleic search, using frame_plus_p2n model
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US-10-649-902-18081
US-11-189-279-64
US-11-189-279-64
US-10-519-335-37
US-10-649-902-17095
US-10-449-902-10702
US-10-449-902-10702
US-10-449-902-1107
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  June 14, 2006, 22:11:12
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Match 1
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Database :

No No Result

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Minimum DB 8 Maximum DB 8

Searched:

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US-10-49-902-17095
US-10-449-902-17095

US-10-449-902-17095

Sequence 17095, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-30

PRIOR PRIOR DATE: 2003-05-30

PRIOR PRIOR DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17095

LENGTH: 2553
                                                               1051 ATGGGGATATTGTGGGGCCCCCTCTGCTCCAGGTTCCCGGTTGCAACTCT 1104
                                     1 MetLysValleuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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US-09-827-854A-13 (1-18) x US-10-953-349-22323 (1-1503)
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                                                                                                                                                                   Sequence 64, Application US/11189279;
Publication No. US20060115829A1
GENERAL INFORMATION:
APPLICANT: MAO, LI
APPLICANT: MAO, LI
APPLICANT: MAO, NAO
TITLE OF INVENTION: A METHOD OF TREATING CANCER
TITLE OF INVENTION: A METHOD OF TREATING CANCER
FILE REPERENCE: UTXC:875US
CURRENT PELING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 60/598,554
PRIOR APPLICATION UNMBER: 60/598,554
PRIOR PILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTING DATE: 2004-08-03
SOFTWARE: PATENTING DATE: 2004-08-03
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Matches:
Conservative:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK067558
DATABASE ENTRY DATE: 2001-12-06
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46.7%
52.2%
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Best Local Similarity:
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LENGTH: 118899
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Pred. No.:
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DB:
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FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                        GAPPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: To Institute of Physical and Chemical Research.
TILE OF INVENTION: FOULL-ENGHTH PLANT CONA AND USES THEREOF
FILE REFERENCE: MOA-NO205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-20369
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 18081
LENTH: 3440
458 GITCTGTGGGTTGCTTTGTTACTATGTTTTTTGTTCATGT 499
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                              Sequence 18081, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: AK068492
DATABASE ENTRY DATE: 2001-12-06
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44.4*
52.2*
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50.00
71.4
64.3
54.3
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ORGANISM: Oryza sativa
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US-10-953-349-22323
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 1503
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NAME/KEY: misc feature
LOCATION: (119024)..(119052)
OTHER INFORMATION: n = a or c or g or t
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LOCATION: (5363)..(5363)
OTHER INFORMATION: n = a or c or g or t
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LOCATION: (109125)..(109125)
OTHER INFORMATION: n = a or c or
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LOCATION: (119053)..(119112)
OTHER INFORMATION: n = a or c or
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LOCATION: (143506)..(143506)
OTHER INFORMATION: n = a or c or
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LOCATION: (109094)..(109094)
OTHER INFORMATION: n = a or c or
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LOCATION: (142063)..(142063)
OTHER INFORMATION: n = a or c or
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LOCATION: (142137)..(142137)
OTHER INFORMATION: n = a or c or
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LOCATION: (142967)..(142967)
OTHER INFORMATION: n = a or c or
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LOCATION: (143077)...(143077)
OTHER INFORMATION: n = a or c or
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LOCATION: (118900)..(118900)
OTHER INFORMATION: n = a or c
    LOCATION: (108055)..(108055)
OTHER INFORMATION: n = a or c
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LOCATION: (119115)..(119121)
OTHER INFORMATION: n = a or
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LOCATION: (141674)..(141674)
OTHER INFORMATION: n = a or
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LOCATION: (143629)..(143629)
OTHER INFORMATION: n = a or
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LOCATION: (119123)..(119123)
OTHER INFORMATION: n = a or
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LOCATION: (143587)..(143587)
OTHER INFORMATION: n = a or
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LOCATION: (149079)..(149079)
OTHER INFORMATION: n = a or
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NAME/KEY: misc feature
LOCATION: (8080)..(8080)
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APPLICANT: Cavarec, Laurent
APPLICANT: Cavarec, Laurent
APPLICANT: Cavarec, Laurent
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Betanaves, Benoit
APPLICANT: Gonthier, Catherine
APPLICANT: Elias, Isabelle
APPLICANT: Blas, Isabelle
APPLICANT: TREATMENT OF MENTAL DISORDERS
FILE OF INVENTION: TREATMENT OF MENTAL DISORDERS
FILE REFERENCE: G-194US03PCT
CURRENT APPLICATION NUMBER: US/10/519,335
PRIOR PILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/391,359
PRIOR FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
LENGTH: 151830
                                                                                                                                                                                                        1105 AIGTCATTGATATGGATGGGCTTGGTGGTAACATACCTCACCGGTGCAGGTGCT 1158
                                                                                                                                                                            1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
                                                                                                                                    US-09-827-854A-13 (1-18) x US-10-449-902-17095 (1-2553)
Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc_feature
LOCATION: (982\overline)..(982\overline)
OTHER INFORMATION: n = a or c or g or t
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LOCATION: (99743)..(99743)
OTHER INFORMATION: n = a or c or g or t
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OTHER INFORMATION: n = a or c or g or t
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LOCATION: (61110) ..(61110)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98209)..(98209)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98210)..(98210)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98211)..(98211)
OTHER INFORMATION: n = a or c or g
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; Sequence 37, Application US/10519335
; Publication No. US2006009210A1
; GENERAL INFORMATION:
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LOCATION: (98207)..(98207)
OTHER INFORMATION: n = a or c
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51.1%
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                  Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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Matches:
Conservative:
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                                 NAME/KEY: misc feature
LOCATION: (10296)..(10296)
OTHER INFORMATION: n = a or c or g or
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NAME/KEX: misc feature
NACATION: (14528)..(14528)
OTHER INFORMATION: n = a or c or g or
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    OTHER INFORMATION: n = a or c or
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LOCATION: (16316)..(16316)
OTHER INFORMATION: n = a or c
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LOCATION: (16397)..(16397)
OTHER INFORMATION: n = a or c
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LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c
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OTHER INFORMATION: n = a or c
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LOCATION: (57662)..(57662)
OTHER INFORMATION: n = a or
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LOCATION: (125441)..(125605)
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LOCATION: (15336)..(15336)
OTHER INFORMATION: n = a or
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LOCATION: (16288)..(16288)
OTHER INFORMATION: n = a or
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OTHER INFORMATION: n = a or
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LOCATION: (96310)..(96422)
OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 5
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OTHER INFORMATION: exon 1
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OTHER INFORMATION: exon 1
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LOCATION: (16306)..(163
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LOCATION: (15457)..(154
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Score:
Percent Similarity:
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LOCATION: (936
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NAME/KEY: exon
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y Sequence 10702, Application US/10449902

| Sequence 10702, Application US/10449902
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: Proundation for Advancement of International Science.
| TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
| FILE REFERENCE: MOA-A0205YI-US
| CURRENT PILING DATE: 2003-05-19
| PRIOR PELICATION NUMBER: US/10/449,902
| PRIOR PELICATION NUMBER: US/2002-203269
| PRIOR PELICATION NUMBER: US/2002-203269
| PRIOR PELING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 10702
| LENGTH: 1371
                                                                                                                                                                                                                                      US-10-449-902-28383/c

US-10-449-902-28383/c

Sequence 28383 Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TILE REFERENCE: MOA-A0205Y1-US

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-30

PRIOR PRING DATE: 2003-05-30

PRIOR PRING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28383

LENGTH: 586
                                                                                                                                                                      151567 AGGTTGTTGGTGGCGCGATGCCAATGATGTTCTCAGCCGGGTGCCAGGCC 151517
                                                                                                                                 2 LysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
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                                                                                          US-09-827-854A-13 (1-18) x US-10-519-335-37 (1-151830)
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Mismatches:
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Matches:
                                              Gaps:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103825
DATABASE ENTRY DATE: 2002-08-28
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                          Query Match:
DB:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Phygical and Chemical Research.
APPLICANT: The Institute of Phygical and Chemical Research.
APPLICANT: The Institute of Phygical and Chemical Research.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR PLING DATE: 2003-05-29
PRIOR FLING DATE: 2002-05-30
PRIOR FLING DATE: 2002-012-11
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Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 GTCATGTGGACGCCGTCCCAGTTGACGTACTTGGCCGGCTGC 1013
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Publication No. US20060123505A1
GENERAL INFORMATION:
OKGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESION NUMBER: AK108050
DATABASE ENTRY DATE: 2002-08-28
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DATABASE ACCESSION NUMBER: AK059168
DATABASE ENTRY DATE: 2001-12-06
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Best Local Similarity:
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                                                                                                  US-10-449-902-10702
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Pred. No.:
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LENGTH: 1425
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Toundation for Advancement of International Science.
TITLE OF INVENTION: FOLL-LENGHT PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-AO205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-29
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 13084
LENGTH: 2794
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Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 2618
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK100495
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK110432
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.00
81.8%
72.7%
47.8%
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ORGANISM: Oryza sativa
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Best Local Similarity:
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Best Local Similarity:
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Sequence 21037, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGIH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US 2002-203269
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21037
     Sequence 27239, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGIP PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 27239
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Mismatches:
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Matches:
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071336
DATABASE BNTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK102681
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27239
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US-10-449-902-27239
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Pred. No.:
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DB:
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2260

Length:

145

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Sequence 24008, Application US/10449902

| Sequence 24008, Application US/10449902
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: Foundation for Advancement of International Science.
| TITLE OF INVENTION WOA-402051-US|
| CURRENT FILING DATE: 2003-05-29
| PRIOR FILING DATE: 2003-05-20
| PRIOR FILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                              Sequence 1533, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Poundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2002-05-29
CURRENT PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

NUMBER OF SEQ ID NOS: 56791

SOUTHWARE PREMEIL OF THE NOS: 56791
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Matches:
Conservative:
Mismatches:
Indels:
                        Conservative:
Mismatches:
Matches:
                                                                         Indels:
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DATABASE ACCESSION NUMBER: AK065861
DATABASE ENTRY DATE: 2001-12-06
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                        Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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LENGTH: 2265
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Search completed: June 14, 2006, 22:15:10 Job time : 9.12303 secs

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